

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 09:54:28 ; Search time 75 Seconds
(without alignments)
1861.955 Million cell updates/sec

Title: US-10-031-241-35
Perfect score: 5457
Sequence: 1 TIKEMPQPKTFGLKNLPL.....RLWLQQLERKGRYKDVWAG 1048

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq.101002.*
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5457	100.0	1048	22	AA1978
2	5457	100.0	1048	22	AA1985
3	5457	100.0	1048	22	AA1986
4	5457	100.0	1049	21	AA193566
5	5457	100.0	1049	22	AA193566
6	5450	99.9	1048	22	AA193566
7	5449	99.9	1049	22	AA193566
8	5444	99.8	1048	22	AA193566
9	5440	99.7	1048	22	AA193566
10	3154.5	57.8	1085	12	AA11504

11	971.5	17.8	1144	9	AA19334	Expression prod. o
12	968.5	17.7	1150	9	AA19337	Expression prod. o
13	962.5	17.6	1150	9	AA19335	Expression prod. o
14	916.5	16.8	1162	9	AA19336	Expression prod. o
15	906.5	16.6	1132	9	AA19338	Expression prod. o
16	778.5	14.3	678	23	AA197261	Mouse ischaemic co
17	774.5	14.2	678	8	AA1970360	Plasmodium rat 1
18	772.5	14.2	678	8	AA1970578	NADPH cytochrome p
19	769	14.1	679	8	AA1970546	Sequence of rabbit
20	769	14.1	682	22	AA1982516	Rabbit NADH cytoch
21	766	14.0	680	22	AA197786	Human full-length
22	766	14.0	685	22	AA197958	Human contig poly
23	761	13.9	677	22	AA1973901	Human derived cyto
24	761	13.9	677	22	AA1973902	Human derived cyto
25	747	13.7	676	20	AA1942286	Human P450 reducta
26	747	13.7	676	20	AA197398	Human P450 reducta
27	747	13.7	676	23	AA197538	Human P450 cytochr
28	746	13.7	671	14	AA1943583	Human P450 cytochr
29	737.5	13.5	616	20	AA1942287	Human anchorless p
30	737.5	13.5	616	20	AA1942287	Human P450 reducta
31	726	13.3	623	9	AA191339	Expression prod. o
32	725.5	13.3	623	9	AA194462	Drosophila melanog
33	723.5	13.3	1169	16	AA197644	Mitochondrial cyto
34	711.5	13.0	883	20	AA195682	Poppy cytochrome p
35	711.5	13.0	883	20	AA195682	Poppy cytochrome p
36	710.5	13.0	692	14	AA193581	Plant NADPH cytoch
37	709	13.0	697	21	AA1935842	Arabidopsis thalia
38	709	13.0	701	21	AA1935841	Arabidopsis thalia
39	709	13.0	711	21	AA1935840	Arabidopsis thalia
40	705.5	12.9	588	23	AA192056	Helianthus tuberos
41	705.5	12.9	588	23	AA192056	Helianthus tuberos
42	703.5	12.9	704	20	AA196392	Poppy cytochrome p
43	703.5	12.9	852	20	AA195681	Poppy cytochrome p
44	695.5	12.7	712	14	AA193582	Plant NADPH cytoch
45	678	12.4	1429	14	AA194489	Sequence of all or

ALIGNMENTS

RESULT 1	AA1978	AA1978 standard; Protein; 1048 AA.
ID	AA1978	
XX	AA1978	
AC	AA1978	
DT	15-MAY-2001 (first entry)	
XX		
DE	Amino acid sequence of a Bacillus P450 monooxygenase protein.	
XX		
KW	Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.	
XX		
OS	Bacillus megaterium.	
XX		
PN	MO200107630-A1.	
XX		
PD	01-FEB-2001.	
XX		
PF	27-JUL-2000; 2000MO-EB07253.	
XX		
PR	27-JUL-1999; * 99DE-1035115.	
PR	18-NOV-1999; 99DE-1055605.	
PR	22-MAR-2000; 2000DE-1014085.	
XX		
PA	(BAD1) BASF AG.	
XX		
PI	Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;	
PI	Li Q;	
XX		
DR	WPI; 2001-182860/18.	
DR	N-FSDS; AAF54832.	
XX		
PT	Cytochrome P450 monooxygenase for oxidizing organic compounds, useful	

PT especially for converting indole to indigo, has wide substrate range -
 XX Claim 3; Page 35-39; 54pp; German.
 CC The present sequence represents a cytochrome P450 monooxygenase. The
 CC specification describes a modified cytochrome P450 monooxygenase which
 CC can oxidize at least one of the following types of substrates:
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or
 CC optionally substituted cycloalkanes or cycloalkenes. The modified
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole
 CC to indigo and indirubin. However, they may be used to oxidise many
 CC other substrates.
 XX
 SQ Sequence 1048 AA;
 Query Match 100.0%; Score 5457; DB 22; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 ACDESRFDKNSQALKFVRDPAGDGLFTSWTHEKNMKKANHILPFSQAMKGYHAMV 120
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 DB 121 DIAVOLVOKMERLNADEHIEVEDMTRTLTLDTGLCGFNVPNSFYRDPHPFTSMVRA 180
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 DB 181 LDEAMNKLOQANPPDDPAYDENKROFOEDIKYMNLDVDTIDRKASGSDLLTHMNG 240
 QY 241 KDPEGEPLDDENIRYQIITFLIAGHETTSGLSFALYLVKNPHVLQKAAEBAARVLVD 300
 DB 241 KDPEGEPLDDENIRYQIITFLIAGHETTSGLSFALYLVKNPHVLQKAAEBAARVLVD 300
 QY 301 PVPSYKQVKQLKYVGMVINEALRLMPTAPAFSLYAKEDTVLGGEVPLEKGDMLVLLPOL 360
 DB 301 PVPSYKQVKQLKYVGMVINEALRLMPTAPAFSLYAKEDTVLGGEVPLEKGDMLVLLPOL 360
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 DB 361 HRDKTIWGDVDEEPRERFENPSAIPQHAFFKPFNGGQACIGQOFAHLEATLVIGMMLKH 420
 QY 421 FDFEDHTNYELDIKETLTLLKPEGFVVKAKSKKIPLGGIPESTESAKVKAKKENAHT 480
 DB 421 FDFEDHTNYELDIKETLTLLKPEGFVVKAKSKKIPLGGIPESTESAKVKAKKENAHT 480
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 DB 481 PLVLVYGSNMGTAAGTADLADIAMSKGAPQVATLDSHAGNLPREGAVLIVTASYNCHP 540
 QY 541 PDNKKOFVDMTDOASADDEVKGVRSVFCGCDKNMATTYQKPAFDETLAKGAEINADR 600
 DB 541 PDNKKOFVDMTDOASADDEVKGVRSVFCGCDKNMATTYQKPAFDETLAKGAEINADR 600
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 DB 1021 HOVSEADARLMLQOLEKGRYADWAG 1048

RESULT 2
 AAB46855
 ID AAB46855 standard; Protein; 1048 AA.
 XX AAB46855;
 AC AAB46855;
 XX AAB46855;
 DT 02-MAY-2001 (first entry)
 XX
 DE B. megaterium cytochrome P450 monooxygenase BM-3 protein.
 XX
 KW Cytochrome P450 monooxygenase; BM-3; electron donor system; bioreactor;
 XX electron transfer; hydroxylatable fatty acid; fatty acid-monooxygenase.
 OS Bacillus megaterium.
 XX
 PN WO200107573-A1.
 XX
 PD 01-FEB-2001.
 XX
 PP 27-JUL-2000; 2000MO-EP07251.
 PR 27-JUL-1999; 99DE-1035115.
 PR 10-MAR-2000; 2000DE-1011723.
 PA (BADI) BASF AG.
 XX
 XX Hauser B, Schmid RD, Schwaneberg U;
 FI
 DR WPI; 2001-159709/16.
 DR N-PSDB; AAF26268.
 XX

PT Novel electron donor system useful for the production of
 PT omega-hydroxylated fatty acids comprises an inorganic electron sink and
 PT a mediator which enables the electron transfer -
 PT
 XX
 XX Claim 13b; Page 83-86; 94pp; German.

CC This invention describes a novel electron donor system (M1) that
 CC transfers electrons to an enzyme with redox properties comprising an
 CC inorganic, not electrode-bound, electron sink and a mediator which enable
 CC the electron transfer. The invention also describes (1) transferring (M2)
 CC oxygen to a hydrocarbon containing hydrogen donor molecule, where the
 CC hydrogen donor molecule is in a reaction medium comprising the oxygen
 CC transferring enzyme and (M1) in the presence of oxygen and incubating
 CC under suitable reaction conditions; (2) the enzymatic production (M3) of
 CC terminally or subterminally hydroxylated (position omega-1 to omega-4)
 CC fatty acids comprising: (1) mixing a hydroxylatable fatty acid or fatty
 CC acid derivative in the presence of (M1) and cytochrome P450
 CC monooxygenase; and (1i) isolating the hydroxylated product; (3) a
 CC bioreactor useful for the production of omega-hydroxylated fatty acids as
 CC described in (2); and (4) detecting (M4) fatty acid-monooxygenases
 CC comprising: (1) contacting the analyte with a omega-hydroxylatable fatty

CC acid or a derivative comprising a terminal chromophore or fluorescent
 CC label in (M); and (ii) qualitatively or quantitatively detecting the
 CC signal. The invention is useful for the production of omega-hydroxylated
 CC fatty acids and the detection of fatty acid monooxygenases. The
 CC invention provides an alternative electron donor system of enzymes with
 CC redox properties that is cheaper and more efficient, where the enzyme
 CC comprises cytochrome 450.

XX Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

Matches 1048; Conservative 0; Indels 0; Gaps 0;

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 DB 121 DIAVOLVOKKERLNADHIEVPEDMTRLTDITGLCGFNTRFNSFYRDQHPPTTSNVRA 180
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 DB 361 HRDKTIWGDVEEERPERFENPSAIPQAPKPFNGORACICGOOFALHEATLVGMMLKH 420
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 DB 781 EALLEKQAYKEOVLAKSLTMLLELKYKACEMKSEFIALPSIRPYSSISSPRVDEK 840
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 DB 841 QASITTVSVSGEAMSGYGEYKGIASNYLAEIOEGDITTCFISTQSEFTLPKDBETPLIM 900

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 DB 1021 HOVSADARLMLQOLEBKGRYAKDVWAG 1048

RESULT 3

AAAB46856
 ID AAB46856 standard; Protein; 1048 AA.
 XX
 AC AAB46856;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE B. megaterium cytochrome P450 monooxygenase Bm-3 protein.
 XX
 KM Cytochrome P450 monooxygenase; Bm-3; site-specific mutagenesis;
 XX
 OS aliphatic carboxylic acid hydroxylation; fatty acid.
 XX
 FN Bacillus megaterium.
 XX
 PN W0200107574-A2.
 PD
 PD 01-FEB-2001.
 PF 27-JUL-2000; 2000MO-EP07252.
 XX
 PR 27-JUL-1999; 99DE-1035115.
 XX
 PR 10-MAR-2000; 2000DE-1011723.
 XX
 PA (BADI) BASF AG.
 XX
 PI Häner B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
 PT Li Q;
 DR WPI; 2001-159710/16.
 XX
 DR N-PSDB; AAF26324.
 PT
 PT New modified cytochrome P450 mono-oxygenase, useful for producing
 PT hydroxylated aliphatic carboxylic acids and derivatives, has altered
 PT substrate specificity -
 XX
 PS Claim 3; Page 41-45; 49pp; German.
 XX
 XX This invention describes a novel modified cytochrome P450 (I) having, as
 CC a result of site-specific mutagenesis of its substrate-binding domain,
 CC an altered substrate profile, relative to the wild-type, when used for
 CC terminal and/or subterminal enzymatic hydroxylation of aliphatic
 CC carboxylic acids. The invention also describes (1) nucleic acid (II)
 CC encoding (I), and its complement; (2) expression cassette (EC) containing
 CC (II) and control elements; (3) a vector containing at least one EC; (4)
 CC recombinant microorganisms transformed with at least one vector of (3);
 CC and (5) enzymatic production of terminally and/or subterminally
 CC hydroxylated aliphatic carboxylic acids (A) using the microorganisms of
 CC (4), or isolated (1). (I), and recombinant cells that express them, are
 CC used to produce hydroxylated aliphatic carboxylic acids or their
 CC derivatives (esters and amides). (I) have altered substrate specificity,
 CC especially for hydroxylation of 8-12C fatty acids at the omega-1, -2
 CC and/or -3 positions, and may also have increased reactivity and/or
 CC regioselectivity.
 XX
 SO Sequence 1048 AA;

Query Match 100.0%; Score 5457; DB 22; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 DIAVOLVOKMERLNADENIEVPEDMTRLLTDTTGLCGFNFRNSFYRQPHPTTSMVRA 180
Db 121 DIAVOLVOKMERLNADENIEVPEDMTRLLTDTTGLCGFNFRNSFYRQPHPTTSMVRA 180
QY 181 LDEAMNKLQRANPPDDPAVDENKROFOEDIKYMNLDVDTIADRKASGSDLLTHMNG 240
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Db 241 KDPETGEPLDDENIRYQIITFLIAGHETTSGLSPALYFLVKNPHVLQKAEBAARVLVD 300
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Db 361 HRDKTIWGDVVEERPERFENPSAIPQHAFFPFGNGRACIGQOPALHEATLVIGMMLKH 420
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QY 901 VGPSTGVAPFRGFVQARQKQKQSGSLGEAHLFYGCRSPHEDYVYQELLENASQEGITTL 960
Db 901 VGPSTGVAPFRGFVQARQKQKQSGSLGEAHLFYGCRSPHEDYVYQELLENASQEGITTL 960
QY 961 HTAFSRMNPQKTYVQHVMEODGKLLIBLLDQGAHFYICDGSQMAPAVEATLTKSYADV 1020
Db 961 HTAFSRMNPQKTYVQHVMEODGKLLIBLLDQGAHFYICDGSQMAPAVEATLTKSYADV 1020
QY 1021 HOVEADARLMLQOLEEKGRYAKDVWAG 1048
Db 1021 HOVEADARLMLQOLEEKGRYAKDVWAG 1048

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RESULT 4
AA93556
ID AA93556 standard; Protein; 1049 AA.
XX
AC AA93556;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of the P450-BM3 sequence.
XX
KW Terpene; cycloalkene; haem-containing enzyme; mutant; oxidation;
infection; P450-BM3.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Misc-difference 303
FT /note= "Val encoded by GCT"
FT Misc-difference 471
FT /note= "Val encoded by GCA"
XX
XX W0200031273-A2.
XX
PD 02-JUN-2000.
XX
PE 19-NOV-1999; 99MO-GB03873.
XX
PR 19-NOV-1998; 98GB-0025421.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Wong LL, Bell SG, Carmichael AB;
XX
DR WPI; 2000-451679/39.
XX
DR N-PSDB; AAA46648.
XX
PT Process for oxidizing acyclic or cyclic terpenes, cycloalkenes, or
derivatives for preventing or treating infection in human or animal
PT body comprises mutant haem-containing enzyme which has substitution of
PT amino acid in the active site -
XX
XX Disclosure; Page 51-53; 63pp; English.
XX
XX The specification describes a process for oxidizing an acyclic or
cyclic terpene, a cycloalkene, or a derivative. The process comprises
oxidizing the compound with a mutant haem-containing enzyme which
comprises a substitution of an amino acid in the active site by an
amino acid with a less polar side-chain. The process is useful for
oxidizing an acyclic or cyclic terpene, a cycloalkene, or their
derivatives. The process is also useful for producing an oxidation
product useful for preventing or treating infection in a human or
animal body. The present sequence represents the amino acid sequence of
the P450-BM3 sequence. The protein is used to construct enzymes
for use in the process of the invention.
XX
XX Sequence 1049 AA:
QY Query Match 100.0%; Score 5457; DB 21; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TIKEMPOKTFGEKLNPLINTDKPVQALMKIADBELGIFKFAAPGVRTRYLSSORLIKE 60
Db 2 TIKEMPOKTFGEKLNPLINTDKPVQALMKIADBELGIFKFAAPGVRTRYLSSORLIKE 61
QY 61 ACDESREFDKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 120
Db 62 ACDESREFDKNLSQALKFVRDPADGDLFTSWTHEKNWKKAHNILLPSFSQAMKGYHAMMV 121
QY 121 DIAVOLVOKMERLNADENIEVPEDMTRLLTDTTGLCGFNFRNSFYRQPHPTTSMVRA 180

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Db      122 DIAVLQVKMERLNADENHIEVPEDMTRLTLDTTGLCGFNFRFNSFYEDQPHFITSMVRA 181
Qy      181 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIADRKAESGSDLLTHMLNG 240
Db      182 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIADRKAESGSDLLTHMLNG 241
Qy      241 KDBETGEPLDENIRYOITITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEBAARLVLD 300
Db      242 KDBETGEPLDENIRYOITITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEBAARLVLD 301
Qy      301 PVPSTYKQVKOLKTVGMVNLNALKLMPPTAPAFSLYAKEDTVLGGHYPLEKDELMVLI.POL 360
Db      302 PVPSTYKQVKOLKTVGMVNLNALKLMPPTAPAFSLYAKEDTVLGGHYPLEKDELMVLI.POL 361
Qy      361 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMWLKH 420
Db      362 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMWLKH 421
Qy      421 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 480
Db      422 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 481
Qy      481 PLLVLVYGSNMGTABGTARDIADIAKSGFAPQVATLDSHAGNLPREGAVLITVASYNGHP 540
Db      482 PLLVLVYGSNMGTABGTARDIADIAKSGFAPQVATLDSHAGNLPREGAVLITVASYNGHP 541
Qy      541 PDNAKQFVMDLDOASADEVGVSVSGCGDKMMAATYQVAPAFIDETLAKAENADR 600
Db      542 PDNAKQFVMDLDOASADEVGVSVSGCGDKMMAATYQVAPAFIDETLAKAENADR 601
Qy      601 GEADASDDEFGTYEEMREHMSDVAAAFNLDIENSEDNKSTLSLOFDSAADPLAMMG 660
Db      602 GEADASDDEFGTYEEMREHMSDVAAAFNLDIENSEDNKSTLSLOFDSAADPLAMMG 661
Qy      661 AFTSTNVASKELOQPGSARSTRHLEIFLPEKASYQEGDHLGVIPRNYEGIVNRYTARFGL 720
Db      662 AFTSTNVASKELOQPGSARSTRHLEIFLPEKASYQEGDHLGVIPRNYEGIVNRYTARFGL 721
Qy      721 DASQOQLRLEAEERKLALPLAKTVSVLELOVVELLOPVRTOLRMAAATVCPHNVEL 780
Db      722 DASQOQLRLEAEERKLALPLAKTVSVLELOVVELLOPVRTOLRMAAATVCPHNVEL 781
Qy      781 EALLEKQAYKEOVLAKLITMLELEKYRACEMKFSFIALPISIRPVYSSISSPRVDEK 840
Db      782 EALLEKQAYKEOVLAKLITMLELEKYRACEMKFSFIALPISIRPVYSSISSPRVDEK 841
Qy      841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDBETPLIM 900
Db      842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDBETPLIM 901
Qy      901 VGGGTGVAPPRGVQARQKOLKEOGOSIGEAHLVFGCSPHEDVLYQBELNNAOSEGITL 960
Db      902 VGGGTGVAPPRGVQARQKOLKEOGOSIGEAHLVFGCSPHEDVLYQBELNNAOSEGITL 961
Qy      961 HTAFSEMPNPKTYVQHVMEQDGKLELIDOGAHFVICDGSQMAVAEATLTKMSYADV 1020
Db      962 HTAFSEMPNPKTYVQHVMEQDGKLELIDOGAHFVICDGSQMAVAEATLTKMSYADV 1021
Qy      1021 HOVSEADARLMLQOLEBKGRYAKDVWAG 1048
Db      1022 HOVSEADARLMLQOLEBKGRYAKDVWAG 1049

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RESULT 5
AAB31882
ID AAB31882 standard; Protein; 1049 AA.
XX
XX AAB31882;
XX
XX
DT 15-MAY-2001 (first entry)
DE Amino acid sequence of a Bacillus P450 monooxygenase protein.
XX

```

KM      Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
XX
OS      Bacillus megaterium.
XX
PN      W0200107630-A1.
XX
PD      01-FEB-2001.
XX
PF      27-JUL-2000; 2000MO-EP07253.
XX
PR      27-JUL-1999; 99DE-1035115.
PR      18-NOV-1999; 99DE-1055605.
PR      22-MAR-2000; 2000DE-1014085.
XX
PA      (BADI ) BASF AG.
XX
PI      Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI      La Q;
DR      WPI; 2001-182800/18.
XX
PT      Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
PT      especially for converting indole to indigo, has wide substrate range
XX
PS      Disclosure; Page 41-44; 54pp; German.
XX
CC      The present sequence represents a cytochrome P450 monooxygenase. The
CC      specification describes a modified cytochrome P450 monooxygenase which
CC      can oxidize at least one of the following types of substrates:
CC      optionally substituted mono- or poly-cyclic aromatic heterocyclics
CC      containing nitrogen, sulphur or oxygen; optionally substituted mono- or
CC      poly-cyclic aromatics; linear or branched alkanes or alkenes; or
CC      optionally substituted cycloalkanes or cycloalkenes. The modified
CC      cytochrome P450 monooxygenase are specifically used to oxidize indole
CC      to indigo and indorubicin. However, they may be used to oxidise many
CC      other substrates.
XX
SQ      Sequence 1049 AA;
Query Match 100.0%; Score 5457; DB 22; Length 1049;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 TIKEMPOPTFGELKULPLNTDQPVQALMKIDELGEIFKFAPRVRYLSSORLIXE 60
Db      2 TIKEMPOPTFGELKULPLNTDQPVQALMKIDELGEIFKFAPRVRYLSSORLIXE 61
Qy      61 ACDESFRDKLSQALKFVDFADGGLFTSWTHKNNKKAHNILLPSFSQAMKGYHAMV 120
Db      62 ACDESFRDKLSQALKFVDFADGGLFTSWTHKNNKKAHNILLPSFSQAMKGYHAMV 121
Qy      121 DIAVLQVKMERLNADENHIEVPEDMTRLTLDTTGLCGFNFRFNSFYEDQPHFITSMVRA 180
Db      122 DIAVLQVKMERLNADENHIEVPEDMTRLTLDTTGLCGFNFRFNSFYEDQPHFITSMVRA 181
Qy      181 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIADRKAESGSDLLTHMLNG 240
Db      182 LDEAMNKLORANPDPAVDENKROFOEDIKVMNDLVOKIADRKAESGSDLLTHMLNG 241
Qy      241 KDBETGEPLDENIRYOITITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEBAARLVLD 300
Db      242 KDBETGEPLDENIRYOITITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEBAARLVLD 301
Qy      301 PVPSTYKQVKOLKTVGMVNLNALKLMPPTAPAFSLYAKEDTVLGGHYPLEKDELMVLI.POL 360
Db      302 PVPSTYKQVKOLKTVGMVNLNALKLMPPTAPAFSLYAKEDTVLGGHYPLEKDELMVLI.POL 361
Qy      361 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMWLKH 420
Db      362 HRDKTIWGDVEEERPERFENPSAIPQAHFKPFGNGORACIGQGFALHEATVLVGMWLKH 421
Qy      421 FDEEDHTNVELDIKETITLTKPEGFVVKAKSKKIPLGGIPSPSTEQSAKKVKKAEANAHT 480

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Db 422 FDFEDHTNVELDIKETLTLLKPEGFVVKAKSKKIPLGGISPSTEQSAKVKAKKAEANANT 481
Qy 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVATLDSHAGNLPREGAVILVTASYNCHP 540
Db 482 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVATLDSHAGNLPREGAVILVTASYNCHP 541
Qy 541 PDNAKQFVMDLQASADEVKGVRSVFCGDKMATTYQKPAFIDETLAAKGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRSVFCGDKMATTYQKPAFIDETLAAKGAENIADR 601
Qy 601 GEADASDDPEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660
Db 602 GEADASDDPEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 661
Qy 661 AFSTNVASKELOQGSARSTRHLEILPKASVQEGSHLVIPRNGEIVNRVYARFGL 720
Db 662 AFSTNVASKELOQGSARSTRHLEILPKASVQEGSHLVIPRNGEIVNRVYARFGL 721
Qy 721 DASQOIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAKTVCPHKKVEL 780
Db 722 DASQOIRLEAEKEKLAHLPLAKTVSVEELLQYVELQDPVTRTOLRAMAKTVCPHKKVEL 781
Qy 781 EALIEKQAYKEQVLAQRILTMLELEKYPACEMKSESEFALLPSIRPRYSSISSPRVDEK 840
Db 782 EALIEKQAYKEQVLAQRILTMLELEKYPACEMKSESEFALLPSIRPRYSSISSPRVDEK 841
Qy 841 QASITVSVSGEAMSGVEYKGIASNYLAEOEGDTICFISTQSEFTLPKDETPILIM 900
Db 842 QASITVSVSGEAMSGVEYKGIASNYLAEOEGDTICFISTQSEFTLPKDETPILIM 901
Qy 901 VGPSTGVAFFRGFVQARQKQLEQSGSLGEAHLYFGCRSPHEDYLYQBELLENAQSGIITL 960
Db 902 VGPSTGVAFFRGFVQARQKQLEQSGSLGEAHLYFGCRSPHEDYLYQBELLENAQSGIITL 961
Qy 961 HTASRPMNQKTYQVHMEQDGKLLLELDQGAHFTICGSGSQAPAVEKTLKSYADV 1020
Db 962 HTASRPMNQKTYQVHMEQDGKLLLELDQGAHFTICGSGSQAPAVEKTLKSYADV 1021
Qy 1021 HOVEADARLWLOOLEKGRYAKDVWAG 1048
Db 1022 HOVEADARLWLOOLEKGRYAKDVWAG 1049

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RESULT 6
AAB31979 ID AAB31979 standard; Protein; 1048 AA.
AAB31979;
15-MAY-2001 (first entry)
Amino acid sequence of a modified P450 monooxygenase protein.
Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
Bacillus megaterium.
Key Location/Qualifiers
FT Misc-difference 87 /note= "wild type Phe changed to Val"
XX MO2001.07630-A1.
XX 01-FEB-2001.
XX 27-JUL-2000; 2000MO-EP07253.
XX 27-JUL-1999; 99DE-1035115.
XX 18-NOV-1999; 99DE-105605.
XX 22-MAR-2000; 2000DE-1014085.
XX (BADT) BASF AG.
XX

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PI Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R;
PI Li Q;
DR WP; 2001-182800/18.
XX
XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
PT especially for converting indole to indigo, has wide substrate range
PS Claim 5; Page -; 54pp; German.
XX
XX The present sequence represents a modified cytochrome P450 monooxygenase.
CC The specification describes a modified cytochrome P450 monooxygenase
CC which can oxidize at least one of the following types of substrates:
CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
CC poly-cyclic aromatics; linear or branched alkenes or alkenes; or
CC optionally substituted cycloalkanes or cycloalkenes. The modified
CC cytochrome P450 monooxygenase are specifically used to oxidize indole
CC to indigo and indorubicin. However, they may be used to oxidize many
CC other substrates.
CC note: this sequence does not appear in the specification; it was created
CC using information provided.
XX
XX Sequence 1048 AA;
SQ

```

Query Match 99.9%; Score 5450; DB 22; Length 1048;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1047; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 TIKEMPOKTFEGELKNLPLINTDKPVQALMKIADLCEIFKFAFGVTRYLSQRLIKE 60
Db 1 TIKEMPOKTFEGELKNLPLINTDKPVQALMKIADLCEIFKFAFGVTRYLSQRLIKE 60
Qy 61 ACDSERFDKLSQALKVRDPAGDGLFTSWTHEKMKKANILLPSQOAMGYHAMV 120
Db 61 ACDSERFDKLSQALKVRDPAGDGLFTSWTHEKMKKANILLPSQOAMGYHAMV 120
Qy 121 DIAVOLQKMERLNADEHIEVPEDMTRLTDTTGLCGFNRYFNSFYRDOPHPTSMVRA 180
Db 121 DIAVOLQKMERLNADEHIEVPEDMTRLTDTTGLCGFNRYFNSFYRDOPHPTSMVRA 180
Qy 181 LDEAMNKLQRPANPDPAVDENKROFOEDIRYANDLVKIIADRKAQSGDDLLTHMLNG 240
Db 181 LDEAMNKLQRPANPDPAVDENKROFOEDIRYANDLVKIIADRKAQSGDDLLTHMLNG 240
Qy 241 KDPEGTGRLDDENRYOITITFLTAGHETTSGLSFALYFLVKNPVHVOXAABEARVLVD 300
Db 241 KDPEGTGRLDDENRYOITITFLTAGHETTSGLSFALYFLVKNPVHVOXAABEARVLVD 300
Qy 301 PVPSEYKQVKKOLKYGVWLNELRLMPTAPAFSLYAKEDTVLGEYPLEKGDMLVLI.POL 360
Db 301 PVPSEYKQVKKOLKYGVWLNELRLMPTAPAFSLYAKEDTVLGEYPLEKGDMLVLI.POL 360
Qy 361 HRDKTIWGDVEEFPFRFENPSAIPQAHKFPNGGRACIGQOFALHEATLVGMWLK 420
Db 361 HRDKTIWGDVEEFPFRFENPSAIPQAHKFPNGGRACIGQOFALHEATLVGMWLK 420
Qy 421 FDFEDHTNVELDIKETLTLLKPEGFVVKAKSKKIPLGGISPSTEQSAKVKAKKAEANANT 480
Db 421 FDFEDHTNVELDIKETLTLLKPEGFVVKAKSKKIPLGGISPSTEQSAKVKAKKAEANANT 480
Qy 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVATLDSHAGNLPREGAVILVTASYNCHP 540
Db 481 PLVLVYGSNMGTAGTARDLADLADIMSKGFAPOVATLDSHAGNLPREGAVILVTASYNCHP 540
Qy 541 PDNAKQFVMDLQASADEVKGVRSVFCGDKMATTYQKPAFIDETLAAKGAENIADR 600
Db 541 PDNAKQFVMDLQASADEVKGVRSVFCGDKMATTYQKPAFIDETLAAKGAENIADR 600
Qy 601 GEADASDDPEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660
Db 601 GEADASDDPEGTYEEMREHMSDVAAAYFNLDIENSSEDKSTLSIQFVDSAADMPLAKMHG 660

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QY 661 AFSTNVASKELQOPSSARSTRHLEIELPKEASYOEGDHLGVI PRNVEGI VNRVTARFGL 720
DB 661 AFSTNVASKELQOPSSARSTRHLEIELPKEASYOEGDHLGVI PRNVEGI VNRVTARFGL 720
QY 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQVLPVTRTQLRAMAAATVCPPHKVEL 780
DB 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQVLPVTRTQLRAMAAATVCPPHKVEL 780
QY 781 EALLEQAVKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRRYSSISSPRVDEK 840
DB 781 EALLEQAVKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRRYSSISSPRVDEK 840
QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
DB 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
QY 901 VEGGTGVAAPRGVQARKOLKEGOSIGENALYFGCSPHEDYLYOBELENAOSEGITL 960
DB 901 VEGGTGVAAPRGVQARKOLKEGOSIGENALYFGCSPHEDYLYOBELENAOSEGITL 960
QY 961 HTAFSPMPNQKTYVQHVMEODGKLI ELLDOGAHFIYICGDSQOMAPAVEATLMKSYADV 1020
DB 961 HTAFSPMPNQKTYVQHVMEODGKLI ELLDOGAHFIYICGDSQOMAPAVEATLMKSYADV 1020
QY 1021 HQVSEADARLMLQOLEBEKGRYADVMAG 1048
DB 1021 HQVSEADARLMLQOLEBEKGRYADVMAG 1048

RESULT 7

AA72208
AA72208 standard; Protein; 1049 AA.

XX AA72208;

DT 24-APR-2001 (first entry)

DE Bacillus megaterium monooxygenase enzyme homologue, P450BM-3.

XX Monooxygenase enzyme; P450BM-3 homologue; P450cam; oxidation;

KM halogenated aromatic compound; electron transfer; putidaredoxin;

XX putidaredoxin reductase; detoxification.

OS Bacillus megaterium.

XX WO200078973-A1.

PD 28-DEC-2000.

XX 19-JUN-2000; 2000MO-GB02379.

PR 18-JUN-1999; 99GB-0014373.

PA (ISIS-) ISIS INNOVATION LTD.

PI Wong LL, Jones JP;

XX WPI; 2001-071397/08.

DR N-PSDB; AAD02365.

XX New process for detoxifying environments contaminated with halo

PT aromatic compounds comprises treating the affected area with a

XX monooxygenase enzyme -

PS disclosure; Page 32-39; 42pp; English.

XX The present invention relates to a process for enzymatically oxidising

CC the halogenated aromatic compounds such as 1,2-dichlorobenzene,

CC 1,2,4-trichlorobenzene, 3,3'-dichlorobiphenyl or 2,2',4,5,

CC 5'-pentachlorobiphenyl. The process comprises treating the polluted

CC environment with a monooxygenase enzyme. A monooxygenase enzyme, P450cam,

CC and its physiological electron transfer partners, putidaredoxin and

CC putidaredoxin reductase, are used to oxidise the halogenated aromatic

CC compounds. Also mutants of the monooxygenase enzyme with substitutions in
CC the active site have enhanced oxidation activity. The process and the
CC transgenic plant or animal which expresses the monooxygenase enzyme are
CC used for detoxifying the environment polluted with the halo aromatic
CC compounds. The present sequence is a Bacillus megaterium monooxygenase
CC enzyme, P450cam, which is homologous to the monooxygenase
CC enzyme, P450cam.

XX Sequence 1049 AA;

Query Match 99.9%; Score 5449; DB 22; Length 1049;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPQPTFGELKULPLINTDKPVOALMKIADLEGIFKFPAPRVTRYSORLIKE 60
DB 2 TIKEMPQPTFGELKULPLINTDKPVOALMKIADLEGIFKFPAPRVTRYSORLIKE 61
QY 61 ACDESFPDKNLSQLKFVDFADGGLFTSWTEKMKKKNHLLPSPSOQAMKGYHAMV 120
DB 62 ACDESFPDKNLSQLKFVDFADGGLFTSWTEKMKKKNHLLPSPSOQAMKGYHAMV 121
QY 121 DIAVOLVQKMERLNADENIEVEPDMTRLTDLITGLCGFNRYRNSFPDQPHPTTSWRA 180
DB 122 DIAVOLVQKMERLNADENIEVEPDMTRLTDLITGLCGFNRYRNSFPDQPHPTTSWRA 181
QY 181 LDEANMKLORANDDDPAYENKROFQEDIKVNMDDVDKIIADKASGEOSDILLTMLNG 240
DB 182 LDEANMKLORANDDDPAYENKROFQEDIKVNMDDVDKIIADKASGEOSDILLTMLNG 241
QY 241 KOPETGEPLDENIRYQITITFLIAGHETTSGLSFLAYELVKNPHYLQKAEBAARVLD 300
DB 242 KOPETGEPLDENIRYQITITFLIAGHETTSGLSFLAYELVKNPHYLQKAEBAARVLD 301
QY 301 PVPSTYQVQKQKTVGNVNLBALRLMPTAPAPSLYAKEDTVLGEYPLEKDELMVLI 360
DB 302 PVPSTYQVQKQKTVGNVNLBALRLMPTAPAPSLYAKEDTVLGEYPLEKDELMVLI 361
QY 361 HRDKTWGDDVEEFRRERENPSAIPQHAFKPRGNQORACIGQFPLHEATVLGMKLK 420
DB 362 HRDKTWGDDVEEFRRERENPSAIPQHAFKPRGNQORACIGQFPLHEATVLGMKLK 421
QY 421 FDFEDHTNYELDKETITLKEGTVKAKSKKIPLOGISPSTEQSAKKARKKAENAHNT 480
DB 422 FDFEDHTNYELDKETITLKEGTVKAKSKKIPLOGISPSTEQSAKKARKKAENAHNT 481
QY 481 PLIVLYGSMNGTAGTARDLADIAMSKGAPQVATLDISHAGNLPREGAVLITVASYNGHP 540
DB 482 PLIVLYGSMNGTAGTARDLADIAMSKGAPQVATLDISHAGNLPREGAVLITVASYNGHP 541
QY 541 PDNAKQFVMDLOASADDEVKGVYVFGCGDKRMATTYQVPAFIDETTLAKAENIADR 600
DB 542 PDNAKQFVMDLOASADDEVKGVYVFGCGDKRMATTYQVPAFIDETTLAKAENIADR 601
QY 601 GEADASDDPEGTYEERHMSDVAAVFNLDIENSDNKSTLSIQVDSADAPLAKMHG 660
DB 602 GEADASDDPEGTYEERHMSDVAAVFNLDIENSDNKSTLSIQVDSADAPLAKMHG 661
QY 661 AFSTNVASKELQOPSSARSTRHLEIELPKEASYOEGDHLGVI PRNVEGI VNRVTARFGL 720
DB 662 AFSTNVASKELQOPSSARSTRHLEIELPKEASYOEGDHLGVI PRNVEGI VNRVTARFGL 721
QY 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQVLPVTRTQLRAMAAATVCPPHKVEL 780
DB 722 DASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQVLPVTRTQLRAMAAATVCPPHKVEL 781
QY 781 EALLEQAVKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRRYSSISSPRVDEK 840
DB 782 EALLEQAVKEQVLAKRLTLMLELEKYPACEMKFSFIALPSPRRYSSISSPRVDEK 841
QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 900
DB 842 QASITVSVSGEAMSGYGEYKGIASNYLAELQEGDITTCFISTPQSEFTLPKDPETPLIM 901

QY 901 VGPSTGVAAPRGFGVQARKOLKEGOSLGEAHLFGCRSPHEDYLYOELENAOSEGIITL 960
 DB 902 VGPSTGVAAPRGFGVQARKOLKEGOSLGEAHLFGCRSPHEDYLYOELENAOSEGIITL 961
 QY 961 HTAFSRMPNPKTYVGHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1020
 DB 962 HTAFSRMPNPKTYVGHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1021
 QY 1021 HOVSEADARLMLQOLEEKGRAKDVWAG 1048
 DB 1022 HOVSEADARLMLQOLEEKGRAKDVWAG 1049

RESULT 8
 AAB31980
 ID AAB31980 standard; Protein; 1048 AA.
 AC AAB31980;
 DT 15-MAY-2001 (first entry)
 DE Amino acid sequence of a modified P450 monooxygenase protein.
 KM Cytochrome P450 monooxygenase; oxidation; indole; indigo; indorubicin.
 OS Bacillus megaterium.
 PH Key Location/Qualifiers
 FT Misc-difference 87 /note= "wild type phe changed to Val"
 FT Misc-difference 188 /note= "wild type Leu changed to Gln"
 XX W0200107630-A1.
 XX 01-FEB-2001.
 PD 27-JUL-2000; 2000WO-EP07253.
 PF 27-JUL-1999; 99DE-1035115.
 PR 18-NOV-1999; 99DE-1055605.
 PR 22-MAR-2000; 2000DE-1014085.
 XX (BADI) BASF AG.
 PA
 XX Hauer B, Pleiss J, Schwaneberg U, Schmitt J, Fischer M, Schmid R,
 PI Li Q,
 PT WPI; 2001-182800/18.
 DR
 XX Cytochrome P450 monooxygenase for oxidizing organic compounds, useful
 PT especially for converting indole to indigo, has wide substrate range
 XX
 PS Claim 5; Page -; 54pp; German.
 XX The present sequence represents a modified cytochrome P450 monooxygenase.
 CC The specification describes a modified cytochrome P450 monooxygenase
 CC which can oxidize at least one of the following types of substrates:
 CC optionally substituted mono- or poly-cyclic aromatic heterocyclics
 CC containing nitrogen, sulphur or oxygen; optionally substituted mono- or
 CC poly-cyclic aromatics; linear or branched alkanes or alkenes; or
 CC optionally substituted cycloalkanes or cycloalkenes. The modified
 CC cytochrome P450 monooxygenase are specifically used to oxidize indole
 CC to indigo and indorubicin. However, they may be used to oxidise many
 CC other substrates.
 CC note: this sequence does not appear in the specification; it was created
 CC using information provided.
 XX
 SQ Sequence 1048 AA;

Query Match 99.8%; Score 5444; DB 22; Length 1048;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFEGKLNPLINTDTPVQALMKIADLGEIEFKFAPGVTRYSLSORLIKE 60
 DB 1 TIKEMPOKTFEGKLNPLINTDTPVQALMKIADLGEIEFKFAPGVTRYSLSORLIKE 60
 QY 61 ACDESREDFKLSQALKFVRDPAGDGLFTSWTHEKMKKKAHNIILPFSQAMKGYHAMV 120
 DB 61 ACDESREDFKLSQALKFVRDPAGDGLFTSWTHEKMKKKAHNIILPFSQAMKGYHAMV 120
 QY 121 DIAVOLYQKWERLNADHEIIVPEDMTRLTIDTGLCGFNRFNSFPRDQPHPTTSVRA 180
 DB 121 DIAVOLYQKWERLNADHEIIVPEDMTRLTIDTGLCGFNRFNSFPRDQPHPTTSVRA 180
 QY 181 LDEAMNKLOKRPANDDPPAYDENKROFOEDIKVMNDLVDKIADKASGEGSDLLTHMLNG 240
 DB 181 LDEAMNKLOKRPANDDPPAYDENKROFOEDIKVMNDLVDKIADKASGEGSDLLTHMLNG 240
 QY 241 KDPETGEPIDDENIRYQIITFLIAGHETTSGLISFALYPLVKNPHYLQKAAEBAARVLVD 300
 DB 241 KDPETGEPIDDENIRYQIITFLIAGHETTSGLISFALYPLVKNPHYLQKAAEBAARVLVD 300
 QY 301 PVSYSYQVQKOLKTYGVNVLNEMALNPTAPAFSLYAKEDTVLGEYPLEKDELMVLIPL 360
 DB 301 PVSYSYQVQKOLKTYGVNVLNEMALNPTAPAFSLYAKEDTVLGEYPLEKDELMVLIPL 360
 QY 361 HRDKTIWGDVVEEFPFRFENPSAIPQAHKPPGNGORACIGQOFALHEATLVLMGLKH 420
 DB 361 HRDKTIWGDVVEEFPFRFENPSAIPQAHKPPGNGORACIGQOFALHEATLVLMGLKH 420
 QY 421 FDEEDHTNYELDIKETLLTKPEGFVYKAKSKKIPLGDISPSTEQSAKKVKKAEVNAHNT 480
 DB 421 FDEEDHTNYELDIKETLLTKPEGFVYKAKSKKIPLGDISPSTEQSAKKVKKAEVNAHNT 480
 QY 481 PLVLVGSNMGTBAGTRADLADLAMSCKFAPQVATLDSHAGNIPRECAVLIIVASVNGHP 540
 DB 481 PLVLVGSNMGTBAGTRADLADLAMSCKFAPQVATLDSHAGNIPRECAVLIIVASVNGHP 540
 QY 541 PDNAKQFVMDLDOASADEVGVRSYFGCGDKMATTYQVPAFIDETLLAAKGAENIADR 600
 DB 541 PDNAKQFVMDLDOASADEVGVRSYFGCGDKMATTYQVPAFIDETLLAAKGAENIADR 600
 QY 601 GEADASDDEFGTYEEMREHMSDVAAVFNLDIENSEBKNSTLSLQFVDSAADMLAMHG 660
 DB 601 GEADASDDEFGTYEEMREHMSDVAAVFNLDIENSEBKNSTLSLQFVDSAADMLAMHG 660
 QY 661 AFSTNVVASKELDQPGSARSTRLEIELPREASVQEGDHGVIIPRNEGIVNVTARFGL 720
 DB 661 AFSTNVVASKELDQPGSARSTRLEIELPREASVQEGDHGVIIPRNEGIVNVTARFGL 720
 QY 721 DASQOIRLEAEEKEKLAHLPLAKTVSVBELQVYELQDPVTRTOLRAMAAKTVCPPHKEVL 780
 DB 721 DASQOIRLEAEEKEKLAHLPLAKTVSVBELQVYELQDPVTRTOLRAMAAKTVCPPHKEVL 780
 QY 781 EALLEKQAYKEQVLAKRLTMLLELEKYPACEMKFSERIALLPISIRPRYSISSPRVDEK 840
 DB 781 EALLEKQAYKEQVLAKRLTMLLELEKYPACEMKFSERIALLPISIRPRYSISSPRVDEK 840
 QY 841 QASITVSVSGEAMSGGEGFKGASNYLALQSGDPTTCTISIPQSFPTLPKPEPTPLIM 900
 DB 841 QASITVSVSGEAMSGGEGFKGASNYLALQSGDPTTCTISIPQSFPTLPKPEPTPLIM 900
 QY 901 VGPSTGVAAPRGFGVQARKOLKEGOSLGEAHLFGCRSPHEDYLYOELENAOSEGIITL 960
 DB 901 VGPSTGVAAPRGFGVQARKOLKEGOSLGEAHLFGCRSPHEDYLYOELENAOSEGIITL 960
 QY 961 HTAFSRMPNPKTYVGHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1020
 DB 961 HTAFSRMPNPKTYVGHVMEODGKKLIELLDQGAHFYICGDSQMAVAEATLMKSYADV 1020
 QY 1021 HOVSEADARLMLQOLEEKGRAKDVWAG 1048
 DB 1021 HOVSEADARLMLQOLEEKGRAKDVWAG 1048

DE P450 17-alpha/P450 BM-3 fusion protein.
 XX bovine adrenal; cytochrome P450; oxidase; reductase; steroid;
 KM plasmid p(alphabM1).
 XX JF03061490-A.
 XX 18-MAR-1991.
 PD 28-JUL-1989; 89JP-0197296.
 XX 28-JUL-1989; 89JP-0197296.
 PR 28-JUL-1989; 89JP-0197296.
 XX (SUMO) SUMITOMO CHEM IND KK.
 PA WPI; 1991-121848/17.
 XX N-PSDB; AA011474.
 DR P450 reductase fused oxidase coding gene - has both mono-atomic
 PT oxygenation activity of bovine adrenal cytochrome p450 17-alpha
 PT and reductivity supplying activity
 XX
 PS Claim 1; Fig 2; 8pp; Japanese.
 XX
 CC The protein is a fusion of bovine adrenal cytochrome P450 17-alpha
 CC and Bacillus megaterium-derived cytochrome P450 BM-3. The fusion
 CC protein has the monatomic oxygenation activity of the former and
 CC the reductivity supplying activity of the latter. Plasmid p(alphabM1),
 CC containing the recombinant sequence encoding the fusion protein, is
 CC used to transform *Saccharomyces cerevisiae*. The transformant is
 CC designated AH22(p(alphabM-1)) and can be used for the synthesis of
 CC steroids.
 XX
 SQ Sequence 1085 AA;
 Query Match 57.8%; Score 3154.5; DB 12; Length 1085;
 Best Local Similarity 60.9%; Pred. No. 1.2e-211;
 Matches 672; Conservative 105; Mismatches 222; Indels 105; Gaps 21;
 QY 3 KEMPQPTFGELKXKPLPLNTDKPQVALMKIADLGEIFKFEAPGRVRYVSSQRLKEAC 62
 DB 29 RSLPSLPLVGSLLPPLP-RAGQOHKNFPLQEKYGPISFRLSGTYVMIGHQOLAREV- 85
 QY 63 DESRFDKXLSQALKFVNDPAG-----DGLFTSWTEKXMKKXANILLPSFS 108
 DB 86 -----LKKKGFSGRPKVALTDLISDNQKGAFA-DIGAHQOLKRLALNAFA 133
 QY 109 QQANKGTHAMVAVQVQKMERLNADH--IEVPRDTRLTLDITGLCGVYRNSF 165
 DB 134 --LFRKDGTLKLEKTIQNEANVLCDFLATQHEAIDLSEPLIAVNTIISFICFNFSPKN- 190
 QY 166 YRDQPHPTSMVVALDENAMKLOKANDPDPAVDENKQFOEDT----- 209
 DB 191 -----EDPALKAIQVN--DGLILEVLSKEVLLDIFPVUKITPSSKAMEMK 233
 QY 210 ---KVMNDLVDKITADRKASGEOSDLDLTHMLN-----GKDEPTEGLDENI---RY 256
 DB 234 GCYQTRNELNBEIL--EKCGENFSDSITNLHLILQAKVADNMMNGRPDDSKLSNRH 291
 QY 257 QITR---FLIGHETTSGLSFALYLVKPNHVLQKAAEBAARVL-VDVPSYQVQKOLK 312
 DB 292 MLATIGDIFGAGVETTSVIMKIVAYLHPSLKKRIODDIDQIIGFRRTFISDRNLV 351
 QY 313 YGVAVNLAEALWLPAPAFSLY-AKEDTVLGEVPLEKDELMVLIPLQHLHDKTIWGDV 371
 DB 352 LLENTINEVLKIRPAPFTLPHKAVIDSSI-GDLTIDGTIVVAVNLALHSEKEM-CHP 409
 QY 372 EEPFRPERENPSAI---POHAFKFGNGORACIGQOPALHEATLVGLMKHDFE--- 424
 DB 410 DLFWPERLDPTGQLISPSLSYLPFGAGPRSGVEMARQELFLFMSRLLOFNLLEIPD 469
 QY 425 DHTVIEDIKETTLTKPEGVVAKAKSKKIPIGGIPSPETESAKVKRKAENANHTPLL 484

DB 470 DGKLPISLEGHASVLQIKPEKXKIEVRQ-----AKREAQAGSGTPEGTAENANHTPLL 522
 QY 485 LYGSNMGTAGCTARDLADIMSKGAPQVATLDSHAGNLPRGAVLITVASYNCHPPDNA 544
 DB 523 LYGSNMGTAGCTARDLADIMSKGAPQVATLDSHAGNLPRGAVLITVASYNCHPPDNA 582
 QY 545 KQFVMDLOASADEVKGRVSVFECGDKMATTYQKVPAPIDETLAKAGENIADRGAD 604
 DB 583 KQFVMDLOASADEVKGRVSVFECGDKMATTYQKVPAPIDETLAKAGENIADRGAD 642
 QY 605 ASDDFEGTYEENKHMMSDVAAAFPNLDIENSEDNKSTLSQFVDSADMDPLAKHGAFT 664
 DB 643 ASDDFEGTYEENKHMMSDVAAAFGLDIENSEDNKSTLSQFVDSADMDPLAKHGAFT 702
 QY 665 NVVASKELQPGSARSTRHLEIELPKESAYQEGDHLGVIPRNEGYVNRVTARFGDASQ 724
 DB 703 NVVASKELQPGSARSTRHLEIELPKESAYQEGDHLGVIPRNEGYVNRVTARFGDASQ 762
 QY 725 QIRLEAEERKLALPLAKTVSVEELLQYVELQDPVTRTQURAMAAKTVCPPHKELEALL 784
 DB 763 QIRLEAEERKLALPLAKTVSVEELLQYVELQDPVTRTQURAMAAKTVCPPHKELEALL 822
 QY 785 EKQAYKQVUAKLTMLELEKYPACEMKSEFTIALPSTRPRYSSSPRVDEKQAST 844
 DB 823 EKQAYKQVUAKLTMLELEKYPACEMKSEFTIALPSTRPRYSSSPRVDEKQAST 882
 QY 845 TVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDEFTLIMWPG 904
 DB 883 TVSVSGEAMSGYGEYKGIASNYLAELQEGDTITCFSTPQSEFTLPKDEFTLIMWPG 942
 QY 905 TGVAFFRGVQARKOLKEQGSJGEAHLVFGCSPHEDYLYQSELENAQSEGIITLTAT 964
 DB 943 TGVAFFRGVQARKOLKEQGSJGEAHLVFGCSPHEDYLYQSELENAQSEGIITLTAT 1002
 QY 965 SRMPNOKTVQVQVMEQDGKLIELDQGANFTICGGSGQMAVAVETLTKSVADYQVS 1024
 DB 1003 SRMPNOKTVQVQVMEQDGKLIELDQGANFTICGGSGQMAVAVETLTKSVADYQVS 1062
 QY 1025 EADARLWLOOLEEKGRYAKDVWAG 1048
 DB 1063 EADARLWLOOLEEKGRYAKDVWAG 1085

RESULT 11
 AAP81334
 ID AAP81334 standard; protein; 1144 AA.
 XX AAP81334;
 AC 19-OCT-1990 (first entry)
 DT 19-OCT-1990 (first entry)
 XX
 DE Expression prod. of plasmid pAMP19.
 XX
 KM Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
 KW industrial waste.
 XX JF63044888-A.
 PD 25-FEB-1988.
 XX 12-AUG-1986; 86JP-0187713.
 PF 12-AUG-1986; 86JP-0187713.
 XX 12-AUG-1986; 86JP-0187713.
 PR (AGEN) AGENCY OF IND SCI TECH.
 XX
 PA WPI; 1988-094816/14.
 DR N-PSDB; AAN81743.
 XX
 PT Chimeric fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
 PT and NADPH-cytochrome p-450 reduction enzyme
 XX
 PS Disclosure; ; P; Japanese.

XX See also AAN81744-48.
 CC XX
 SQ Sequence 1144 AA;
 Query Match 17.8%; Score 971.5; DB 9; Length 1144;
 Best Local Similarity 28.3%; Pred. No. 7,4e-59;
 Matches 320; Conservative 186; Mismatches 468; Indels 157; Gaps 43;
 25 PVQALMKIADLEGEIFKFEAPGRTVRLSSQRLKEACDSRFDKLSQALKFVRDPAQD 84
 DB PHLSLTKLSQOYGDVQLIRIGSTPVVLSGLNTIKQA-----LVKQGDDEKGR 110
 63 GLFTSWTHEKN-----WKKAHNILLPSFQOAMKGY-----HA 117
 85 GLFTSWTHEKN-----WKKAHNILLPSFQOAMKGY-----HA 117
 DB PDLYSFTLLANGOSMTFNDPSGFLMAARRL-----AQNMLKSFJASDPTLASCYLEE 165
 111 PDLYSFTLLANGOSMTFNDPSGFLMAARRL-----AQNMLKSFJASDPTLASCYLEE 165
 QY 118 MMYDIAVOLVOKERLNAD-EHIEVEDMTRLTLDTIGLCGFNYRNSFYRDOPHPFITS 176
 DB HVSKEAEYLISKQKLMABEVGHDPFKYLVSVANVICAICFGRRD--HDDQELLSTVN 223
 166 HVSKEAEYLISKQKLMABEVGHDPFKYLVSVANVICAICFGRRD--HDDQELLSTVN 223
 QY 177 MYRALDEAMNK-----LQRPND--DPAVDENKROFQEDIKVNNDLVDKIIADRKA 225
 DB 224 LSNFEGSVTGSYPADFTILRLPNSSLDAFKDLNKKFY-----SFMKLIIKHYR 275
 224 LSNFEGSVTGSYPADFTILRLPNSSLDAFKDLNKKFY-----SFMKLIIKHYR 275
 QY 226 SGRQ-----SDLLTLMNGK--DPEGEPLDENIRYOIITFLIAGHETTSGLSPALY 278
 DB 276 TFEKGHRIOTDLSLIEHCQRRLDENANNVQLSDKVTIYFDLFGAGFDITTAISWSLM 335
 276 TFEKGHRIOTDLSLIEHCQRRLDENANNVQLSDKVTIYFDLFGAGFDITTAISWSLM 335
 QY 279 FLVKNPHVLQKAEEARVL--VDPVPSYKQVKQLKYGVNVLNEALRLMPTAPAFSL--YA 335
 DB 336 YLVTNPRIORKIOBELDTVIGRDRQRLSDRQPLFEALFLETFRHSFVP--FTIPHS 394
 336 YLVTNPRIORKIOBELDTVIGRDRQRLSDRQPLFEALFLETFRHSFVP--FTIPHS 394
 QY 336 KEDTVLGEVPLKDEBLMLLIPQLHRDKTIMGDVVEEPPEPENS-AIPQAFRP-- 392
 DB 395 IRDTSLNGFY-IRKGHCVFNQOVNHDQELMDP--NEFRPERLISGTLDKHLSKVI 452
 395 IRDTSLNGFY-IRKGHCVFNQOVNHDQELMDP--NEFRPERLISGTLDKHLSKVI 452
 QY 393 -FGNGORACIGQOFALHEATLVLMMLKHPDEPHTYELDIKET--LTLPK--EGFVV 446
 DB 453 LFLGLGRKCIIGETIGRLVEFLFLAILLOQMEFNVSPEKXDMTPAYGLTIKARCHEFQV 512
 453 LFLGLGRKCIIGETIGRLVEFLFLAILLOQMEFNVSPEKXDMTPAYGLTIKARCHEFQV 512
 QY 447 KAKSK--KIPLGIPSPSTEQOS-AKKVKKAEVNAHNTPLVLYGSNNGTAEGTARDLAD 503
 DB 513 QMRSSGPRAMIQTAPPVKESSFEKMKKTGRN-----IIVFGSSQGTAEFEFANRLSKD 567
 513 QMRSSGPRAMIQTAPPVKESSFEKMKKTGRN-----IIVFGSSQGTAEFEFANRLSKD 567
 QY 504 AMSKGFAPQVATIDSH---AGNLPR--EGAVLITVASY--NGHPNDAKQFVMDLQASA 556
 DB 568 AHRVGMKMSADPEEYDLADLSLPEIDKSLVVFQWATYEGDPTDNAODFYVWLQETDV 627
 568 AHRVGMKMSADPEEYDLADLSLPEIDKSLVVFQWATYEGDPTDNAODFYVWLQETDV 627
 QY 557 DEKGVYRVSFGCGDKMATTYQKVP--FIDETLLAKGAENIADGADADDFEGTY 613
 DB 628 D-LTGKVFAYFGIGNK---TYEHFNAMKQVDOQLQOLQORIFELGLDDEGNEEDF 682
 628 D-LTGKVFAYFGIGNK---TYEHFNAMKQVDOQLQOLQORIFELGLDDEGNEEDF 682
 QY 614 EEMREHMSDVAAYFNLDIENSNDKSTLSLQFVDSADMPAKM----- 659
 DB 683 ITRREQFWPAPVCEPFGVATGEESIRQVELVME--DMDVAKVYVYGMGRLSKYENOK 739
 683 ITRREQFWPAPVCEPFGVATGEESIRQVELVME--DMDVAKVYVYGMGRLSKYENOK 739
 QY 660 -----GAFSTNVASGELOQPGASRSTRLEIEL-PKEASVQBGHLYGIPRYBEIYN 712
 DB 740 PEPDANKPFLAAVYANKLNQ--GTERHLMHLELDISDSKIRYBSGDSVAAYPANDSALVN 798
 740 PEPDANKPFLAAVYANKLNQ--GTERHLMHLELDISDSKIRYBSGDSVAAYPANDSALVN 798
 QY 713 RVTARFG--LDASQOIRLEAEEKLAHLPLAKTVSVELLOYVLODPVTRTOLRAAAK 770
 DB 799 QIGELIAGADIVMSLNNDDEESNKGIPFCPTTYRALTYYLDTINP--RTINVLVLAQ 857
 799 QIGELIAGADIVMSLNNDDEESNKGIPFCPTTYRALTYYLDTINP--RTINVLVLAQ 857
 QY 771 TVCP-----HKVELEALLKQAYKQVLAKRLTMLLEKKYPACEMKSEFALLPSI 824
 DB 858 YASEPSEOEHLHKMASSSGGKELYLSMVVEARHILAILQDYPSLRPPIDLCELLPRL 917
 858 YASEPSEOEHLHKMASSSGGKELYLSMVVEARHILAILQDYPSLRPPIDLCELLPRL 917
 QY 825 RPRYTSISSPRVDEKASITVSVSGEAMSGYGEYGIASNYL--ALQGGDT-----IT 878
 DB 918 QARYSTIASSKVPNSVHICAVAVEYEAQSGRVN--KGVATSWLRAPAGEGNGRALVP 976
 918 QARYSTIASSKVPNSVHICAVAVEYEAQSGRVN--KGVATSWLRAPAGEGNGRALVP 976

QY 879 CFISTPQSEFTLPEKDEETPLINVGPGTGVAPFPGFVQARKOLKEQSGSLGEAHLVYGCRS 938
 DB 977 MFVR--KSQGRLPFKSTTPVIMVGPCTGIAPFWMGFIQERAMLEBQGEVGETLLVYGCRR 1034
 977 MFVR--KSQGRLPFKSTTPVIMVGPCTGIAPFWMGFIQERAMLEBQGEVGETLLVYGCRR 1034
 QY 939 PHEDIYQSELENAQSEGIIT-LHTAFSRMPNPKTYVQVHMQDQKLLIELDQ--GAF 996
 DB 1035 SDDYLYREELARFHDQGLTQLVNAFSR--EQAHKYVQHLILRDEHMLKLIHEGGAHI 1093
 1035 SDDYLYREELARFHDQGLTQLVNAFSR--EQAHKYVQHLILRDEHMLKLIHEGGAHI 1093
 QY 997 YICGDSQMAPAYEATLMSYADVQVSEADARLMLQOLEEKGRYAKDWVA 1047
 DB 1094 YVCGDARNNAKDQVNTFYDIVAEFGPMHTQADVYKKLMTKGRYSLDWS 1144
 1094 YVCGDARNNAKDQVNTFYDIVAEFGPMHTQADVYKKLMTKGRYSLDWS 1144
 RESULT 12
 AAP81337
 ID AAP81337 standard; protein; 1150 AA.
 XX
 AC AAP81337;
 XX
 DT 19-OCT-1990 (first entry)
 XX
 DE Expression prod. of plasmid pALP25.
 XX
 KW Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
 KW industrial waste.
 XX
 PN JP63044888-A.
 XX
 PD 25-FEB-1988.
 XX
 PF 12-AUG-1986; 86UP-0187713.
 XX
 PR 12-AUG-1986; 86UP-0187713.
 XX
 PA (AGEN) AGENCY OF IND SCI TECH.
 XX
 DR WPI; 1988-094816/14.
 XX
 N-PSDB; AAN81746.
 XX
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
 PT and NADPH-cytochrome p-450 reduction enzyme
 XX
 PS Disclosure; ; p; Japanese.
 XX
 CC See also AAN81743-85 and AAN81747-48.
 CC
 SQ Sequence 1150 AA;
 Query Match 17.7%; Score 968.5; DB 9; Length 1150;
 Best Local Similarity 28.1%; Pred. No. 1.2e-58;
 Matches 320; Conservative 166; Mismatches 468; Indels 163; Gaps 43;
 25 PVQALMKIADLEGEIFKFEAPGRTVRLSSQRLKEACDSRFDKLSQALKFVRDPAQD 84
 DB PHLSLTKLSQOYGDVQLIRIGSTPVVLSGLNTIKQA-----LVKQGDDEKGR 110
 63 GLFTSWTHEKN-----WKKAHNILLPSFQOAMKGY-----HA 117
 85 GLFTSWTHEKN-----WKKAHNILLPSFQOAMKGY-----HA 117
 DB PDLYSFTLLANGOSMTFNDPSGFLMAARRL-----AQNMLKSFJASDPTLASCYLEE 165
 111 PDLYSFTLLANGOSMTFNDPSGFLMAARRL-----AQNMLKSFJASDPTLASCYLEE 165
 QY 118 MMYDIAVOLVOKERLNAD-EHIEVEDMTRLTLDTIGLCGFNYRNSFYRDOPHPFITS 176
 DB 166 HVSKEAEYLISKQKLMABEVGHDPFKYLVSVANVICAICFGRRD--HDDQELLSTVN 223
 166 HVSKEAEYLISKQKLMABEVGHDPFKYLVSVANVICAICFGRRD--HDDQELLSTVN 223
 QY 177 MYRALDEAMNK-----LQRPND--DPAVDENKROFQEDIKVNNDLVDKIIADRKA 225
 DB 224 LSNFEGSVTGSYPADFTILRLPNSSLDAFKDLNKKFY-----SFMKLIIKHYR 275
 224 LSNFEGSVTGSYPADFTILRLPNSSLDAFKDLNKKFY-----SFMKLIIKHYR 275
 QY 226 SGRQ-----SDLLTLMNGK--DPEGEPLDENIRYOIITFLIAGHETTSGLSPALY 278
 DB 276 TFEKGHRIOTDLSLIEHCQRRLDENANNVQLSDKVTIYFDLFGAGFDITTAISWSLM 335
 276 TFEKGHRIOTDLSLIEHCQRRLDENANNVQLSDKVTIYFDLFGAGFDITTAISWSLM 335
 QY 279 FLVKNPHVLQKAEEARVL--VDPVPSYKQVKQLKYGVNVLNEALRLMPTAPAFSL--YA 335
 279 FLVKNPHVLQKAEEARVL--VDPVPSYKQVKQLKYGVNVLNEALRLMPTAPAFSL--YA 335

QY 707 YEGIVNVTARFG--LDASQOIRLEAESEKLAHLPLAKTVSVEELLQYVELODPVTRTOL 764
 DB 799 DSALVNQIGELLGADLVIMSLNLDSESNKGFPCPTTYRTALTYLDTINP-PRTNV 857
 QY 765 RAMAAKTVCP-----HKVELEALLKQAYKEOVLAKRLTLMLELEKYPACEMKFSFPI 818
 DB 858 LYELAQVASEPSEOEHLHKAASSSGEKELEYLSWVVEARRHIILALDQYSLRPIIDHLC 917
 QY 819 ALPSIRPRYYSISSSPRVDEKQASITVSVSGEAMSGYGEYKGIASNYL-AELQEGDT- 876
 DB 918 ELPLRLARYSIASSSKVHPNSVHICAVAVEYAKSGRVN-KGVAISMLPAKPAENG 976
 QY 877 -ITCFISTPOSEFTLPKDPETPLIMVGPSTGVAFRFGVQARKOLKEGQSLGEAHL 932
 DB 977 GRALVMEFVR--KSQFRLPFKSTTPVIMVGPSTGVAFRFGVQARKOLKEGQSLGEAHL 1034
 QY 933 YFGCRSHEDYLYOELEENAOSEGIT-LHTAFSRMPNPKTYQVHMEODGKLLIELLD 991
 DB 1035 YGGRSRDEEDYLYEELARFKDQALQNLVAFPR-EQAHKVVYQHLKEDREHLMKLIH 1093
 QY 992 Q-GAHFYICGDSQMAPAVEATLMKSYADVHQSADARLMLQOLEBKGRAXQVMA 1047
 DB 1094 EGGHITVCGDARMMAKOVQNTFYDVAEFGEMHTQAVDVKLMTKGRISLDVWS 1150

RESULT 14

ID AAP81336 standard; protein; 1162 AA.
 AAP81336

XX AC AAP81336;
 XX DT 19-OCT-1990 (first entry)
 DE Expression prod. of plasmid pALP17.
 KM Cytochrome P450; NADPH cytochrome P-450; reduction; oxidation;
 KW Industrial waste.
 XX JF63044888-A.
 XX PD 25-FEB-1988.
 XX PF 12-AUG-1986; 86JP-0187713;
 XX PR 12-AUG-1986; 86JP-0187713.
 XX PA (AGEN) AGENCY OF IND SCI TECH.
 XX DR WPI; 1988-094816/14.
 XX DR N-PDB; AAN81745.
 PT Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome P-450
 XX and NADPH-cytochrome P-450 reduction enzyme
 PS Disclosure; ; P; Japanese.
 XX See also AAN81743-84 and AAN81746-48.
 XX SQ Sequence 1162 AA;

Query Match 16.8%; Score 916.5; DB 9; Length 1162;
 Best Local Similarity 27.2%; Pred. No. 5.3e-55;
 Matches 314; Conservative 185; Mismatches 469; Indels 187; Gaps 43;
 QY 25 PVQAMKIALDELGEIFEFKAPRVTRKLSORLIKEACDSRPDKNISQALKFYRPAQD 84
 DB 63 PHSLTTLSSQYGVDLQIRIGSTPVVVLISGLNTIKQA-----LVKQGDDEPKGR 110
 QY 85 GLFTSMTEHKN-----WKAHNIILPSFQOAMKGY-----HA 117
 DB 111 PDLYSTFLINAGQSMNTNPDGSLMAARRL-----AQNALKSFSTIASDPTLASSCYLEE 165

QY 118 MVDIAVOLVQKMERLNAD-EHIEVEDMTRLTLDTGLCGFNVRNFSFYRQDPHPFITS 176
 DB 166 HVSKEAEYLSKQKMAEYGHDFPFKYLVSVANVICAICFGRVD--HDDQELLSTVN 223
 QY 177 MVALDEANMK-----LQANPD--DPAYDENKQFOEDIKVMNDLVKIIADRA 225
 DB 224 LSNFEGEVNGSGYPADFIPLIRYLPNSSLDAFDLNNKFY-----SFMKLIKHYR 275
 QY 226 SGEQ-----SDLLTHMLNGK--DPETGEPLDDENIROYIITFLIGHETSGLSALY 278
 DB 276 TFEKGHRTIDTDLIEHCQDRLDENANVOLSDCKYITTFDLPAGAFDTITTAISWSLM 335
 QY 279 FLVKNPVLQAKAEARVVL-VDPVSYKQVKOLKTYGWLNALRLMPAPAFSL--YA 335
 DB 336 YLVTRNRQIKQIEBLDTVIGRDRPRLSDRPLPIEAAILTFTRHSSVTP-FTIPHST 394
 QY 336 KEDTVLGGYPLKQGBLWVLIPLQHRDKTIWDDVVEEFPFEPENDS-AIPQHAEPK- 392
 DB 395 IRDTSLNGFY-IRKQGVFNQWQVNHDDQELMGDP-NEFPFEPFLTSSGTLDKHLSKVI 452
 QY 393 -FNGSORACIGQGFALHEATLVLMMLKHPFEDHNTYELDIKET--LTIKP--EGFVY 446
 DB 453 LPELGRKRCIGETIGRLEVFLLALILQMEFNVSPEEKVMDPAYGLTLKHARCEHFQV 512
 QY 447 KAKSKKIPLQGLIPSPSTEOGA-----KVKRKAENAHNT 480
 DB 513 QMRS-----SGRPSAAARSAARSAARSAARMIQTAPPVKSSFVEKMKTKGRN----- 563
 QY 481 PLIVLYGSMNGTAEGRADLADIAMSGKFAPOVATLDSH--AGNLPR--EBAVLIVTA 534
 DB 564 -IIVFGSQTGTAEERANRLSKDHRVGMKGMADEEYDLADLSLPEIDKLVFQMA 622
 QY 535 SY-NGHPDNQKQVFMVMDASADEVKVARYSVFSGGDKMATTYQKVP--FIETTLA 590
 DB 623 TYEGDPTDAQOFYVMLQETDVD-LTGVAFAVGLGNK--TYHFNMKGTYVQORLE 677
 QY 591 AKGAENIADRGADASDDEGTVEEWRHMSDVAAVFNLDIENSEDNKSTLSLQEFDSA 650
 DB 678 QLGAGRIIFELGLDDDGDNLEEDFTWRBOFWPAVCFEYGEATGESSITQYLVVHE-- 735
 QY 651 ADMPLAKM-----GASTNVVASKELQOPGASRSTRLEIEL-P 689
 DB 736 -DMDVAKVYTGEMGRKLSYENQKPPDANKPFLAAVTANKLNQ-GTERHMLHLEIDISD 793
 QY 690 KEASYOEGHLYGTPNNESGIYVNVYARFG--LDASQOIRLEAESEKLAHLPLAKTVSVE 747
 DB 794 SKIRYESGDHVAAYPANDSALVNQIGELGADLVIMSLNLDSESNKGFPCPTTYRT 853
 QY 748 ELQYVELDPVYRTOLRAMAAKTVCP-----HKVELEALLKQAYKEOVLAKRLTLM 801
 DB 854 ALTYVYLDITNP-PRTNVLYELAEYASEPSEOEHLHKAASSSGEKELEYLSWVVEARRHL 912
 QY 802 ELLEKYPACEMKFSFPIALIPSIIRPRYYSISSSPRVDEKQASITVSVSGEAMSGYGEYK 861
 DB 913 AIIQDYPSLRPIIDHCELPRLQARYYSIASSSKVHPNSVHICAVAVEYAKSGRVN-K 971
 QY 862 GIASNYL-AELQEGDT-----ITCFISTPOSEFTLPKDPETPLIMVGPSTGVAFRFGVQ 915
 DB 972 GVATSWLRAPKAPENGGRALVMEFVR--KSQFRLPFKSTTPVIMVGPSTGVAFRFGVQ 1029
 QY 916 ARKOLKEGQSLGEAHLFYGCRSPHEDYLYOELEENAOSEGIT-LHTAFSRMPNPKTY 974
 DB 1030 ERMWLEQGEVETILLYGCRSDSDYLYREBLARFKDQALQNLVAFSRSDSDYLY 1089
 QY 975 VQHV--MEODGKLLIELDOGAHFYICGDSQMAPAVEATLMKSYADVHQSADARLML 1032
 DB 1090 REELARFHXDG--ALQNLVAFSIVCGDARMMAKOVQNTFYDVAEFGEMHTQAVDVY 1147
 QY 1033 OOLEEGRYAKQVMA 1047
 DB 1148 KLMTKGRISLDVWS 1162

```

RESULT 15.
AAP81338
ID AAP81338 standard; protein; 1132 AA.
XX
AC AAP81338;
XX
DT 19-OCT-1990 (first entry)
DE Expression prod. of plasmid pALP4.
XX
KM Cytochrome p450; NADPH cytochrome p-450; reduction; oxidation;
XX industrial waste.
XX JPe3044888-A.
XX
PD 25-FEB-1988.
XX
PF 12-AUG-1986; 86JP-0187713.
XX
PR 12-AUG-1986; 86JP-0187713.
XX
PA (AGEN ) AGENCY OF IND SCI TECH.
XX
XX WPI; 1988-094816/14.
XX DR N-PSDB; AAN81747.
XX
XX Chimera fusion enzyme gene - coding oxidation enzyme of cytochrome p-450
XX and NADPH-cytochrome p-450 reduction enzyme
XX
XX Disclosure; ; Japanese.
XX
XX See also AAN81743-86and AAN81748.
XX
SQ Sequence 1132 AA;

Query Match 16.6%; Score 906.5; DB 9; Length 1132;
Best Local Similarity 27.2%; Pred. No. 2.6e-54;
Matches 308; Conservative 187; Mismatches 464; Indels 175; Gaps 44;

25 PVQALMKIADLGEIFKFEAPGRVTRVYSQRLTKKACDESRFDKNLSQALKFVDFPGD 84
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
63 PHLSTKLSQQYGDVLRIGSTPVVLSGNTIKQA-----LVKQGDDEKGR 110
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

85 GLFTSWTHEKN-----WKANHILLSFSQAMKGY-----HA 117
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
111 PDVLSFTLIANGQSTWNPDSGPLMAARRL-----AGNALKSPSIADPTLASSCYLSE 165
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
118 MMVDIAVQVQKMERLNAD-EHIEVEDMTRLTDTGLCGNRYRNSFYRDQHPPTTS 176
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
166 HVSKEAEYLISKFOKLMAEVGHFDPFKYLVSVANVICAICFGRYD--HDDQELISIVN 223
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
177 MVRALDEAMNK-----LORAND---DPAVDENKQFOEDIKVMNDLVDKIADKA 225
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
224 LSNREGVETGGYPADFPILRKYLPNSSLDAPKDLNKKFY-----SPMKULKEHYR 275
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
226 SGEQ-----SDDLITHLNKGK-DPETGEPLDENIRYQITFLIAGHETTSGLISFALY 278
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
276 TFEKGHIRDITDSLEHQCQRLDENANVQSLDDKVIITIVDFGAGFDITTTAISWSLM 335
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
279 FLVKNPHTVLOKAAEEAARVL-VDPVSYKQVKQLKYGVMLNEALRLMPTAPASL--YA 335
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
336 YLVNTPRIQRKIQEELDTVIGRDRPRLSDRPQRLYLEAFILFTFRHSSFPV-FTIPHS 394
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
336 KEDTVLGEYVLEKDELMVLLPOLHRDKITWGDVEEFPREPERFNP-S-ALPOLAFK-- 392
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
395 IRDTSLSNGFY-IPKHCVFNQWQVNDHDELWGP-NFRRPRFLTSSGTLDKHLSKOM 452
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
393 ---FGNGORACIGQOFALHEATLVLMMLKHFDEFDHTNYELDIKETLLTKPEGFV--- 446
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
453 EFNNSPGEK-----DWTIPAGLTLKARCE--HFQVQWSSS---GPRAAAAADRA 497
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
447 -----KAKSKKIPLGGIPSPSTEGS-AKVRKKAENAHNTPLVLVYGSNMGTAEGTADL 500
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db 498 AAADRAAADRAMIQTAPPVKSSSFVEKMKKTGRN-----IIVFGSQGTAEFANRL 552
Oy 501 ADIAMSGFAPQVATLDSH---AGNLPR--EGAVILVITASY-NGHPDPAKQFVDWLDQ 553
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 553 SKDAHRYGIRGMADPEEYDLADLSLPEIDKSLVFCMAITYGEGPTDAQDFYDWLQE 612
Oy 554 ASADENVKRVYVFGCGDKXMAWTTQKQVPA--FIDETLAKGAENIADRGADASDFE 610
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 613 TDVD-LTGVAFAVFGLENK---TYEHFNAMGKYVDRLQGLAQRIFFELGLDDDDNLE 667
Oy 611 GTYEEMREHMSDVAAFENLDIENSEDNKSTLSLQFVDSAADPPLAMH----- 659
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 668 EDFITWREQFWPAVCEFFGVEATGEBSIRQYELVHE---DMDVAVVYGENGRKLSYE 724
Oy 660 -----GAFSTNVVASKELOPGSARSTRHLEIL-PKASVYORGDHLGVIPRYEG 709
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 725 NQKPPPAKNPFLAAVTAANKLNQ-GTERILMHELDISDSKIRYESGDHVAAYPANDSA 783
Oy 710 IYNRVTAIFG--LDASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQVLPVTRTQLRAM 767
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 784 LVNQIGETILGADLDVIMSLNNLDESNKKHPCPCPTTYRTATLVYLDITNP-PRTNVLYE 842
Oy 768 AAKTVCP-----HKVELALBEKQAYKEQVLAKLTMLELEKYPACEMKSEFIALL 821
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 843 LAQYASPESEOEHLKXVASSGEGKELYLSWVVEARRHILAILQDVPSLRPIDHLCCELL 902
Oy 822 PSIRPRVYSSISPRVDEKQASITVSVSGEAMSGYGEYGIASNYL-AELOEGDT----- 876
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 903 PRLOARYTSLASSSKHPNSVHICAVAVEYKASGRN-KGVATSWLRAEPAGENGRA 961
Oy 877 -ITCFISTPQSEFTLPKDPETPLIMVGPSTGVAPFRGFGVQARKOLKEQOGLGBAHLFYG 935
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 962 LVPMFVR--KSQFLRPFKSTTPVIMVGPSTGVIAPEFMGFIQERAMLRQGEVETLLYYG 1019
Oy 936 CRSPHEHYLQOELENAQSGIIT-LHTASRPKNQKTVQVQHMEDGKKLLIELLDQ-G 993
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1020 CRSDDEDYLYREBELARPHKQDGLQLNVAFSR-EQAHKVYVQHLKKDRHLMKLIHEGG 1078
Oy 994 AHFYICGDSQMAPAVEATLMKSYADVHGVSEADARLMLQOLEBKGRYADVMA 1047
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1079 AHIVCGDARMAKDVONTFYDVAERGPMEHQAVDYVKKLMTKGRISLDVMS 1132

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Search completed: May 29, 2003, 10:04:08
Job time : 82 secs

Db 300 LALAAHSDATEADRLQFLASREKDEYAEWIVANORSLLEWMEAFPSAKPEPLGVFPAI 359
 QY 821 LPSIRPYVSTSSPRVDEKQASTIVSVSGEAMSGVGEYKIASNY-----LAEIOEG 874
 Db 360 APRIOPRYVSTSSSPKVPNRIRHVTCALVY-EKTPGGRIRHKGICSTWMAKNAVLTENDOC 418
 QY 875 DTITCFISTPOSEFTLPKDPETPLIMVPGTVAFFRGFVQARKOLKEOGSLGEAHLVF 934
 Db 419 SSADIFVRT--SNRRLPADRPVPIIMIGPTGLAPFGFLOERLALAKESGTELQSTLEFF 476
 QY 935 GCRPHEDYLYQOELENAQSGCITT-LHTAFSRNPQKTYVQVYMEDQKKLIELDDOG 993
 Db 477 GCRNRKXDFIYENLNFVENGALSELDMAFSR-EGASKEYVQHKMSQKADINMMLSEG 535
 QY 994 AHFICGDSQMAVAEATLMKSYADVHQVSEADARLMLQOLEKGRYAKDVW 1046
 Db 536 AYLVCGDAKMADVHRTHTIVQEGNLDSKAELYVKNLQMSGRYLRDW 588

RESULT 2

US-07-642-002-2
 ; Sequence 2, Application US/07642002
 ; Patent No. 5268465
 ; GENERAL INFORMATION:
 ; APPLICANT: Bredt, David S.
 ; APPLICANT: Hwang, Paul M.
 ; APPLICANT: Reed, Randall
 ; APPLICANT: Snyder, Solomon H.
 ; TITLE OF INVENTION: Purification and Molecular Cloning of Nitric
 ; TITLE OF INVENTION: Oxide Synthase
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner, Birch, McKie & Beckett
 ; STREET: One Thomas Circle, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/642.002
 ; FILING DATE: 19910118
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kagan, Sarah A.
 ; REGISTRATION NUMBER: 32,141
 ; REFERENCE/DOCKET NUMBER: 1107.033576
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 296-5560
 ; TELEFAX: (202) 296-7830
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1429 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-642-002-2

Query Match 12.4%; Score 678; DB 1; Length 1429;

Best Local Similarity 28.2%; Pred. No. 2.6e-50;

Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

QY 457 GIPSPSTEQSAKKVKKAE-----NAHNTPLVLVYGSNMGTAEGTADLADIA 504
 Db 718 GTNGTPTGRRAIGFKLAFAVFSKLMGQMAKVKATIIYAEETGSGQAVAKTLCEIF 777
 QY 505 MSKGFAPQVATLDSAGLPRREGANLITYASY-NQHPDNMAKQF-----547
 Db 778 KHAFDKAMSMEEYDVLHLEHALVLTSTFGNDPENEKEFGCALMEMRHPNSVOEE 837

QY 548 -----VDMLDQ-ASADEKGVRYVFCGDKMATTYQKVP 582
 Db 838 KSKYKRFNSVSSYSDSRKSSGGDPLRDINFESTGTPLANRFRVFLGSGR-----AVPHFC 893
 QY 583 AF--IDETLAAGAENIADRGAADSDDEFTYEEMREHMSDVAAYPNL--DIENSED 637
 Db 894 AFGHAVDTLLIEELGGERILMRGDELCQGEAFRTMAKKVFAACDVFCEVDVNIKEP 953
 QY 638 NKSTLS-----LOFVDSADMP--LAQMH--GASTVWVAASKELQOPGASRSTR 682
 Db 954 NNSLISNDRSKWKRFRLTYVAEPDTQGLSNVHKRVSANRLSHONLQSPFSRSTI 1013
 QY 683 HLEIEL--PREASVQEGDHLGVIPIRVYEGIVNVTARF--GLDASQOIRLEAESEKLAHL 738
 Db 1014 FVRLHTNGNELQYQPDHGVFPGNHEDLVNLIIELEDPAPPANVYKEMLEERTAL 1073
 QY 739 PLAKTVSEELL-----QVLEQDPVTRTQLRANAAKTVCPRHVLEALLE-KQ 787
 Db 1074 GVISNMKDESRLLPCTTFQAFKYVLDITTPPTPLQLOQFASLATNEKORLLVLSKGLQ 1133
 QY 788 AYKEQVLAKRLTLELEKYPACEMKFSERIALPSIRPYVSTSSSPRVDEKQASTIVS 847
 Db 1134 EYEBWKKGKPTWVELEEFPSIQMPATLLTLQSLQPPRYVSTSSPDVYPRDEHILTV 1193
 QY 848 VSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPOSEFTLPKDPETPLIMVPGTG 906
 Db 1194 IVSYHTRDGEQPVNHHGVCSWLMNRIQADVPCFVGAPS-FILPRNPQPCILVGGTG 1252
 QY 907 VAPPRGFVQARK-QLKEQOSLGEAHLVFCGRPHEDYLYQOELENAQSGCII-TLHTAF 964
 Db 1253 IAPFRSFWQOROPDIQHKGNPCPMVLVFCRCROSKI DHIYREBTLQKNGVRELYTAY 1312
 QY 965 SRNPQKTYVQVYMEDQKKLI--ELLDOGAFFYICGDSQMAVAEATLMKSYADVHQ 1022
 Db 1313 SREEDRPKTYVDVLQGLAESYRALKEQGGHIVCGDVTMAADVUKA-IQRIIMQOGK 1371
 QY 1023 VSEADARLMLQOLEKGRYAKDVW 1046
 Db 1372 LSEEDAGVFISRLRDNDRYHEDIF 1395

RESULT 3

US-08-365-486A-13
 ; Sequence 13, Application US/08365486A
 ; Patent No. 5634306
 ; GENERAL INFORMATION:
 ; APPLICANT: Webster, Keith A.
 ; APPLICANT: Bishopric, Nanette H.
 ; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 ; TITLE OF INVENTION: Therapeutic Constructs
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/365.486A
 ; FILING DATE: 23-DEC-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 8255-0018
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1429 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-365-486A-13

Query Match 12.4%; Score 678; DB 2; Length 1429;
 Best Local Similarity 28.2%; Pred. No. 2,6e-50;
 Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

457 GIPSPSTEQSAKKVRKAE-----NAHNPPLVLVYGSNMGTAEGTARDLADIA 504
 DB 718 GTNGTPTKRRALGFKKLAEVKSASAKMGQAMAKRYKATILVATETGKSOAVAKTLCIEIF 777
 QY 505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF-----547
 DB 778 KAFADAKAMSEMEYDILVHLEHALVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVOEE 837
 QY 548 -----VDMLDQ-ASADVKGVRYVFGCGDKMATTYQKVP 582
 DB 838 RKSXYKRFNSVSSYSRSKSSGGDPLRDNFESTGPLANVRFSVFGIGSR----AYPHFC 893
 QY 583 AF---IDETLAAGANINADRGEDASDDEGTYEERHMSDVAAVFNL--DIENSED 637
 DB 894 AFQHAVDTLLELIGERILKMRGDELCOGEAFRTMAKVFRAACDVCVGDVNIKRP 953
 QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQCGSARSTR 682
 DB 954 NNSLISNDSSWKNNKFRLLTVAAAPDLTQGLSNVHKRVSAARLLSRONQSKFRSTI 1013
 QY 683 HLEIEL--PREASVYQGDHLGVIPRYVEGIVNRVTARF--GLDASQOIRLEAEKLAHL 738
 DB 1014 FVRLHTNGOELQYQGDHLGVFPNGHEDLVNALIERLEDAPPANHVKVMLEERNTAL 1073
 QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKVCPPHKYLEALLE-KQ 787
 DB 1074 GVISNMKDSRLPPCTIFQAFKYLLDTITPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133
 QY 788 AYKEQVLAKLRLTMLELEKYPACEMKFSERIALLPISIRRYVSISSSPRDEKQASITVS 847
 DB 1134 EYEWKMGKNNPTMVELEEFPSIQMPATILLLTQLSLQRPYVSISSSPMDVPRDEVHLTVA 1193
 QY 848 VVSGEAMSGYE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPCTG 906
 DB 1194 IVSYHTRDEGFPVHGVCSMMLNRIOADDVAPCFVGRAPS-FHLPNPPQVPCILVGPCTG 1252
 QY 907 VAPFRGFVQARK-QLKEQGSLSBAHLVFCGRSPHEDYLVOELENNASGII-THTAF 964
 DB 1253 IAFRRFPWQORQDIOHKGNPCPMVLVFGCRQSKIDHIREETLQAKNGVFRRELYTAY 1312
 QY 965 SRAPNPKTYVQVHMEODGKKLI--ELVDGAFYILYICGDSQMAPAVEATLMSYADVHQ 1022
 DB 1313 SRPDPKPKTYVQVLOQLAESYRALKEGGHHIYCGDVTMAADVILKA-IQIMTQCGK 1371
 QY 1023 VSEADARLMLQOLEKGRVAKDVA 1046
 DB 1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 4
 US-08-319-866-11

; Sequence 11, Application US/08319866
 ; Patent No. 5929223

; GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.

; APPLICANT: Yim, Jerry C.

; APPLICANT: Regulski, Michael

; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES

; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY

NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,866
 FILING DATE: 7-OCT-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL94-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-9540
 TELEFAX: (617) 861-6240
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1429 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-319-866-11

Query Match 12.4%; Score 678; DB 2; Length 1429;
 Best Local Similarity 28.2%; Pred. No. 2,6e-50;
 Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;

457 GIPSPSTEQSAKKVRKAE-----NAHNPPLVLVYGSNMGTAEGTARDLADIA 504
 DB 718 GTNGTPTKRRALGFKKLAEVKSASAKMGQAMAKRYKATILVATETGKSOAVAKTLCIEIF 777
 QY 505 MSKGFAPQVATLDSHAGNLPREGAVLIVTASY-NGHPPDNAKOF-----547
 DB 778 KAFADAKAMSEMEYDILVHLEHALVLVVTSTFGNGDPPENGEKFGCALMEMRHPNSVOEE 837
 QY 548 -----VDMLDQ-ASADVKGVRYVFGCGDKMATTYQKVP 582
 DB 838 RKSXYKRFNSVSSYSRSKSSGGDPLRDNFESTGPLANVRFSVFGIGSR----AYPHFC 893
 QY 583 AF---IDETLAAGANINADRGEDASDDEGTYEERHMSDVAAVFNL--DIENSED 637
 DB 894 AFQHAVDTLLELIGERILKMRGDELCOGEAFRTMAKVFRAACDVCVGDVNIKRP 953
 QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTNVVASKELQCGSARSTR 682
 DB 954 NNSLISNDSSWKNNKFRLLTVAAAPDLTQGLSNVHKRVSAARLLSRONQSKFRSTI 1013
 QY 683 HLEIEL--PREASVYQGDHLGVIPRYVEGIVNRVTARF--GLDASQOIRLEAEKLAHL 738
 DB 1014 FVRLHTNGOELQYQGDHLGVFPNGHEDLVNALIERLEDAPPANHVKVMLEERNTAL 1073
 QY 739 PLAKTVSVEELL-----QYVELQDPVTRTQLRAMAAKVCPPHKYLEALLE-KQ 787
 DB 1074 GVISNMKDSRLPPCTIFQAFKYLLDTITPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133
 QY 788 AYKEQVLAKLRLTMLELEKYPACEMKFSERIALLPISIRRYVSISSSPRDEKQASITVS 847
 DB 1134 EYEWKMGKNNPTMVELEEFPSIQMPATILLLTQLSLQRPYVSISSSPMDVPRDEVHLTVA 1193
 QY 848 VVSGEAMSGYE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDPETPLIMVGPCTG 906

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Db      1194 IVSYHTRDGEPRVHNGVSSWLNRIQADDDVPCFVRGAPS-FHLPNPOVPCILVGGTGT 1252
Qy      907 VAPRPGVQARK-QLXKOGOSLGEAHLYFGCRSPHEDLYOELENNOSGII-TLHTAF 964
Db      1253 IAPRSTWQORQFDIQHKGNPCPMVLVFGCRSKIDHIREETLOAKNGVRELTYAT 1312
Qy      965 SRMPNPKTYVQVHMEODGKKLI--ELLDGAFHYICGDSGOMAPAVEATLMKSYADVHQ 1022
Db      1313 SREDRKRYVQDVLQGLAESYRALKEGGHIVYCGDVTMADVLKA-IQRIMTQOGK 1371
Qy      1023 VSEADARLWLOOLEEKGRYAKDV 1046
Db      1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 5
US-08-880-342-13
Sequence 13, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1429 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-13

Query Match 12.4%; Score 678; DB 4; Length 1429;
Best Local Similarity 28.2%; Pred. No. 2.6e-50;
Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
Qy      457 GIPSPSTEQSAKKRYKRAE-----NANTPLLVYGSNMGAETADLADIA 504
Db      718 GTNGTPTKRRALIGFKLAEAVKFSAKLMGOMAKRVKATLIVATETGSKQAVATLCEIF 777

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Qy      505 MSKGFAPQVATLDSHAGNLPRGAVLIVTASY-NGHPDNKQOF----- 547
Db      778 KHAFFDAKAMMEYDYVHLEHEALVIVTSTFNGQPRPENGKFGCALMEMRHNVSQOE 837
Qy      548 -----VMDLO-ASADEKGVRYVFGCGDKMATTYQKVP 562
Db      838 RKSYKRVFNSSYSRSKSSCGDPLRDNFESTGPLANRFVFGISR----AYPHFC 893
Qy      583 AF---IDETLAAGANINADRGADASDDPEGVYEEEMRHMWSDVAAYFN---DIENSED 637
Db      894 AFGHADVTLLEBYGKERILMRGDELCOGEAFRTWAKVFAACDVFVGDVNIKRP 953
Qy      638 NKSTLS-----LOFVDSAADMP--LAKCH--GAFSTNVASKELOPGSASTR 682
Db      954 NNSLISNDRSMKRNKFRPLYVAEAPPLTQGLSVHKKRVSAARLLSQNLQSPKFSSTI 1013
Qy      683 HLEIEL--PREASYQEGDHLGVIIPRYEGIVNRYTARF--GLDASQOIRLEAEKLAHL 738
Db      1014 FVRLHTNGNQLQYQGDHLGVFPGNHEDLVNALLERLEDAAPPANHVYKVMLEERTAL 1073
Qy      739 PLAKTVSEELL-----QYVELQDPVTRTOLRAMAKTVCPHKKVLEALLE-KQ 787
Db      1074 GVISMWDESRLEPCTTFQAFKYLLDTTPPTPLQLOQFASLATNEKEKORLLVLSKGLQ 1133
Qy      788 AYEQVLAKRLTMLLELEKYPACEMKFSERIALLPRIPRYVSISSPRVDEKQASITVS 847
Db      1134 EYEMKMKGNKPTVNEVLEEFPSIQMPATLILLTQLSLQPPRYVSISSPMYPRDEHLYVA 1193
Qy      848 VSGEAMSGYGE-YKGIASNYLAELQBGDTITTFISTPOSEFTLPDPETPLIMVGBTG 906
Db      1194 IVSYHTRDGEPRVHNGVSSWLNRIQADDDVPCFVRGAPS-FHLPNPOVPCILVGGTGT 1252
Qy      907 VAPRPGVQARK-QLXKOGOSLGEAHLYFGCRSPHEDLYOELENNOSGII-TLHTAF 964
Db      1253 IAPRSTWQORQFDIQHKGNPCPMVLVFGCRSKIDHIREETLOAKNGVRELTYAT 1312
Qy      965 SRMPNPKTYVQVHMEODGKKLI--ELLDGAFHYICGDSGOMAPAVEATLMKSYADVHQ 1022
Db      1313 SREDRKRYVQDVLQGLAESYRALKEGGHIVYCGDVTMADVLKA-IQRIMTQOGK 1371
Qy      1023 VSEADARLWLOOLEEKGRYAKDV 1046
Db      1372 LSEEDAGVFISRLRDNRYHEDIF 1395

RESULT 6
US-08-705-625-4
Sequence 4, Application US/08705625
Patent No. 5908756
GENERAL INFORMATION:
APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,625
FILING DATE: 30-AUG-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.

```

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?      REGISTRATION NUMBER: 32,141
?      REFERENCE/DOCKET NUMBER: 01107.57071
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: 202-508-9100
?      TELEFAX: 202-508-9299
?      INFORMATION FOR SEQ ID NO: 4:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 1430 amino acids
?      TYPE: amino acid
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      HYPOTHETICAL: NO
?      ORIGINAL SOURCE:
?      ORGANISM: Homo sapiens
?
US-08-705-625-4

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Query Match	12.4%	Score 678;	DB 2;	Length 1430;	
Best Local Similarity	28.2%	Pred. No.2,6e-50;			
Matches	193;	Conservative 126;	Mismatches 265;	Indels 100;	Gaps 20;
Qy	457	GIPSPSTEQSAKKVAKKAE-----	NAHNTPLLVLGSMNGTAEGTARDLADIA	504	
Db	718	GTNGTPTKRRATIGFKKLAEAVKFAKLMGMAMAKVKATITLYATETGSAQYAKTLCEIF		777	
Qy	505	MSKGFAPVALTDSAGNLPBEGAVLITYTASY-KNHPPDNAKQF-----		547	
Db	778	KHAFDAKAMSEEDYIVLHEHALVLTSTFTFGNDPENGNEKFECCALMEMKHPNSVOEE		837	
Qy	548	-----VDWLDQ--ASADEVGVRSVSGCGDKMMATTYQKVP		582	
Db	838	RKSKYKVRPNSSVSSDSKSSGDDGLDNDNEESTPLPNVRFSSVGLSR---AYHPFC		893	
Qy	583	AF----IDETLAKGAENIADRGADASDDEFGTYEEMREHMSDVAAYFNUL--DIENSED		637	
Db	894	AFGNAVDTLJBELGERILTKMRBEGELCGGEAPFTWAKVFKACADVFCVGGDVNIEMK		953	
Qy	638	NKSTLS-----LQFVDSADMP-LAKNH-GAFSTNVVASLQOPGASRSTR		682	
Db	954	NNSLISNDRSMKRNKFRLLTYVAEAPDTLQGLSNVHKKRSAARLSRQNLQSPKFSRSTI		1011	
Qy	683	HLEIEL--PKRASVOEGDHLGVIPNRYNGIYNRVARF--GLDASQOIRLAEEMEKLAHL		738	
Db	1014	FVRLHTNGNQELQYOPGDHLGFPENHEDLVNALLERLEDAPRAHVAVKVELEERNFTAL		1073	
Qy	739	PLAKTVSVEELL-----QVVELDDPVTRTQLRAMAAKTVCPPKHVELEALLE-KQ		787	
Db	1074	GVISNWKDESLRPCTTFQAFKRYUIDTTPRPRLQOPFASLATNEKQRLVLVSKGLQ		1133	
Qy	788	AYKEQVLAKRLTLMLELLEKYPACEMKFSFEIALLPISIRPRYSSISSSPRVDEKQASITVS		847	
Db	1134	EYEMKMKGNKPNVLELFEPSIQMPATILITQLSLQPRYSSISSPDMPDVEHLITVA		1192	
Qy	848	VVSGEAMSGYGE-YKGIASNTVLAIEQEDDTITCFISTQSEETLPKPDETPLIMVPGTG		906	
Db	1194	IVSYHTRDGEPRVHNHGVCSSWMLNRIQADVDVPCFVRGAPS-FHLPRNQVPLIIVPGTG		1252	
Qy	907	VAPPRGFVOAKR-OLKEQGOSLGEAHLYFGGCSPHEDLYOEBELNADSEGI-TLHTAF		964	
Db	1253	IAPRPSFQOQOFDIQHKGNMPCPVLVFGCROSQKIDITHREBTLQAKXKGVFRELLTAY		1312	
Qy	965	SRMENOPTKYVQHWMEODGKKLI--ELLDGAHFYICGDSGOMAPAEATLTKMSYADVHQ		1022	
Db	1313	SREBDRPKKYVDVLYQEOQLASVYALKKEGGHIVVCGDVMAADVLKA-IQRINTQOGK		1371	
Qy	1023	VSEADARLMLQOLEKGRYAKDWM		1046	
Db	1372	LSEEDAGVIFRLRDNRYHEIDF		1395	

```

1 GENERAL INFORMATION:
2 APPLICANT: Snyder, Solomon
3 APPLICANT: Jaffrey, Samie
4 APPLICANT: Snowman, Adele
5 APPLICANT: Eliasson, Mikael
6 APPLICANT: Cohen, No. 6103872m
7 TITLE OF INVENTION: CAPON, a protein that binds
8 TITLE OF INVENTION: neuronal nitric oxide synthase
9 NUMBER OF SEQUENCES: 8
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Banner & Witcoff
12 STREET: 1001 G Street, NW
13 CITY: Washington
14 STATE: DC
15 COUNTRY: USA
16 ZIP: 20001
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FastSeq for Windows Version 2.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/010,998
24 FILING DATE: 22-JAN-1998
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER:
28 FILING DATE:
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Kagan, Sarah A
31 REGISTRATION NUMBER: 32141
32 REFERENCE/DOCKET NUMBER: 01107,73424
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 202-508-9100
35 TELEFAX: 202-508-9299
36 TELEX:
37 INFORMATION FOR SEQ ID NO: 5:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 1430 amino acids
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: No. 6103872e
44 US-09-010-998-5

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RESULT 7
US-09-010-998-5
; Sequence 5, Application US/09010998

Query Match	12.4%	Score 678	DB 3	Length 1430
Best Local Similarity	28.2%	Pred. No. 2.6e-50		
Matches 193	Conservative 126	Mismatches 265	IndeIs 100	Gaps 20
QY	457	GIPSPSTEQSAKKYKKA-----	NAHNTPLLVLVYGSNMGTAEGTADLADIA	504
DB	718	GTGNGPTTRRAIIGPKDLAEVAFSAKLMGQAMAKRVKATILLYATBTGSGQAVAKTLCEIF		777
QY	505	MSKGPAFOVATLDSHAGNLPPREGAVLITYTASY-NGHPDNAKQF-----		547
DB	778	KHADPAKASMEEDYIVLHEEALVLYVTSTFGGNDPPRENGEFCGALMEMHRPNVSQVE		837
QY	548	-----YDMLDQ-ASADEVAGVSIVSYSGGCKDMATTYYQKVP		582
DB	838	RKSYKVRPNVSIVSYSDRSKSGDGPDLKDNFESTGEPPLNANVPSVFGLSR---AYPHFC		893
QY	583	AF--IDETLAKAENIADRGEADASDPDEFGTAEEMREHMSDVAAYFNL--DIENSED		637
DB	894	AFGHAVIDLLEELGGERLTKMRBEGDELCQGEAPRTAKYVFKPACADVFCVGDVDVNIKP		953
QY	638	NKSTLS-----LQFVDSAADNP-LAKQH-GAFTNVVASXELDQPGSARSTR		682
DB	954	NNSLISNDRSKWRNKKFRLLTYVAEPDLQGLSNVHKKRVSAARLLSRONLQSPKFSRSTI		1013
QY	683	HLEIEL--PKASVQEGGHTGVIRPNTGVINRYTARF--GLDASQQRLEAESEKLAHL		738
DB	1014	FVRLITNGNQLOQOPGDHLGAPGQNHEDLVNALERLEDAPRAAHVVKVEMLEERTAL		1077

QY 739 PLAKTVSVEELL-----QYVELQDVTRTOLRAMAKTVCPPHKVELLEALL-E-KQ 787
D 1074 GVISNMKDESRLLPPTCFQAFKYYLIDITPTPTLOQFASLANEKKQRLVLVSKGLQ 1133
QY 788 AYKQVLAKEKLTMLELEKYPACEMKSEFIALPSIRPRYSISSSPRDEKQASTVS 847
D 1134 EYEWKMGKKNPTWVELEEFPSIQMPALTLTOLSLQPRYSISSSPDMYPDEHVLVA 1193
QY 848 VVSGEAMSGYGE--XKGIASNYLAELQEGDITTCFISTPQSEFTLPKDEPTLIMVGPSTG 906
D 1194 IVSHHTDGEPRVHGVSSMLNRIQADVVPCFVRGAPS--FHLPRNQVPCILVGPSTG 1252
QY 907 VAPRGFVOARK--OLKEQOSLGEANLYFGCRSPHEDYLYOELENAQSGII--TLHTAF 964
D 1253 IAPFRSFQOQROFDIOHKGNPCPMVLVFCGRQSKIDHIVREETLQAKNGVRELVTAY 1312
QY 965 SRMNPQRTYVQHVMEQDGKLI--ELLDOGAHFYICGDSQMAPAVEATIMKSYADVHQ 1022
D 1313 SREDRPKKYVQDVLYQELASVYRAKQGGHIVCGDVTMAADVKA--IQIMTQOGK 1371
QY 1023 VSEADARLMLQOLEEKRYAKDV 1046
D 1372 LSEEDAGVFISRLDNRHYHEDIF 1395

RESULT 8

US-09-220-574-4
Sequence 4, Application US/09220574
Patent No. 6168926

GENERAL INFORMATION:

APPLICANT: Snyder, Solomon H.
APPLICANT: Jaffrey, Samie R.
TITLE OF INVENTION: Protein Inhibitor of Neuronal Nitric
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
COUNTRY: U.S.A.
ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220, 574
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705, 625
FILING DATE: 30-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,57071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-220-574-4

Query Match 12.4%; Score 678; DB 4; Length 1430;
Best Local Similarity 28.2%; Pred. No. 2,6e-50;

Matches 193; Conservative 126; Mismatches 265; Indels 100; Gaps 20;
QY 457 GISPSTEQSAKKVKKAE-----NAHNPLVLVYSGNMGTAGTRADLADIA 504
D 718 GTMGPTPKRAIGFKLAIEVKSAKIMGQAKRVKATILVITETGSKQAYAKTLCEIF 777
QY 505 MSKGFAPQVATLDSHAGNLPRGAVLIVTASY--NGHPDNKQF----- 547
D 778 KHAIFDAKAMEEYDIHLEHVALVLTSTFCNGDPPENGEKFGCALMEMRHNSVQEE 837
QY 548 -----VMDLQ--ASADEKVGKRYSVFGGDKMAATTYKVP 582
D 838 RKSXKVFNSVSSYSDRSKSGDGPDLRDNFESTGPLANRVFVFGIGSR---AYPHFC 893
QY 583 AF---IDETLAAGAENIADRGADASDDEPGTYEERHEHMGDVAAFYNL--DIENSED 637
D 894 AFGHAIVTLLEEIGENILMKRGDELCCGEEAFRYAKVFPKACDVFVGDDVNIKP 953
QY 638 NKSTLS-----LOFVDSAADMP--LAKMH--GAFSTVNVASKELQPGSARSTR 682
D 954 NNSLISNDRSMKKNKFRLYVAEAPDLTQGLSNVHKRVGAARLSRONLQSPKFSRTI 1013
QY 683 HLEIEL--PKFASYQSGDHLGVIPRYEGIVNRYTARF--GLDASQIRLEAEKLAHL 738
D 1014 FVRLHTNGNOELOYPQGDHLGVFPNGHEDLVNALIERLEDAPAPNHVVKEMLEERTAL 1073
QY 739 PLAKTVSVEELL-----QYVELQDVTRTOLRAMAKTVCPPHKVELLEALL-E-KQ 787
D 1074 GVISNMKDESRLLPPTCFQAFKYYLIDITPTPTLOQFASLANEKKQRLVLVSKGLQ 1133
QY 788 AYKQVLAKEKLTMLELEKYPACEMKSEFIALPSIRPRYSISSSPRDEKQASTVS 847
D 1134 EYEWKMGKKNPTWVELEEFPSIQMPALTLTOLSLQPRYSISSSPDMYPDEHVLVA 1193
QY 848 VVSGEAMSGYGE--XKGIASNYLAELQEGDITTCFISTPQSEFTLPKDEPTLIMVGPSTG 906
D 1194 IVSHHTDGEPRVHGVSSMLNRIQADVVPCFVRGAPS--FHLPRNQVPCILVGPSTG 1252
QY 907 VAPRGFVOARK--OLKEQOSLGEANLYFGCRSPHEDYLYOELENAQSGII--TLHTAF 964
D 1253 IAPFRSFQOQROFDIOHKGNPCPMVLVFCGRQSKIDHIVREETLQAKNGVRELVTAY 1312
QY 965 SRMNPQRTYVQHVMEQDGKLI--ELLDOGAHFYICGDSQMAPAVEATIMKSYADVHQ 1022
D 1313 SREDRPKKYVQDVLYQELASVYRAKQGGHIVCGDVTMAADVKA--IQIMTQOGK 1371
QY 1023 VSEADARLMLQOLEEKRYAKDV 1046
D 1372 LSEEDAGVFISRLDNRHYHEDIF 1395

RESULT 9

US-08-365-486A-21

Sequence 21, Application US/08365486A
Patent No. 5834306

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1433 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-21

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Query Match 12.4%; Score 675; DB 2; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

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QY 457 GTPSPTEGSAKVRKKAEE-----NAHNPFLVLVYSGNMGTAGTARDLADIA 504
DB 722 GINGTPTKRRALGFKKLAEAVKESAKLMGQAMAKRVKATILVATETGSAQVAKTICEI- 780
QY 505 MSKGPAQVATLDNH-AGNLPREGAVLIVTASY-NGHPDPAKOF-----547
DB 781 FKIAFPAKVMSEBYDIHLEHETLVLVVTSTGNDPPENGKFGCALMEMHPNSVOE 840
QY 548 -----VDWLDQ-ASADEVKGVRYSVFGCGDKMATTYQKV 581
DB 841 ERKSYKVRNVSYSYDSQKSGDGPDLRNFESAGPLANRVSVGLGSR-----AYPHF 896
QY 582 PAF---IDETLAKGAENIADRGEDASDDEFTYEEMREHMSDVAAYNLT--DIENSE 636
DB 897 CAFGHAVDTLLEELGGERILKMEGDELCGQEAFTWAKVFAACDVFCVGDVNIK 956
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQPGSARST 681
DB 957 ANNSLSLNDKSMKRNKFRLLTFVAEAPLTOGLSNVHKRVSAARLSRQNLQSPKSRST 1016
QY 682 RHLEIEL--PKESAYOEGDHLGVLPRNYEGIVNRVTARFGIDA---SQQIRLEAEERK-- 734
DB 1017 IFRRLHTNGSQELQYQPGDHLGVFPGNHEDLVNALIERLE-DAPVNVQWVKELLEERN 1075
QY 735 -----LAHLPLAKTVSEELLQYVELQDPVTRTQLRAMAAKTVCPRHKELEALLE- 785
DB 1076 ALGVISNMTDELRLPCTIFQAFKYVLDITPTPTPLQLOQFASLATSSEKORLLVLSKG 1135
QY 786 KOAYKEQVLAKLRLTMLELEKYPACEMKFEFIALPSIRPRYSSISSSPRVDEKQASIT 845
DB 1136 LOEYEEKMKGNPTIYVELEEFPSIQMPATLLTQLSLQLOPRYSSISSSDMPDPDEVHLT 1195
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDITTCISTPOSEFTLPKDETPPLINWPG 904
DB 1196 VALVSVTRTRGEGEPIHHGVCSWLNRIQADELVPCFVRGAPF-FHLPRNQVPCILVPG 1254
QY 905 TGVAAPRGRVQARK-OLKEQOGSLGEANHYFGCRSPHEDVLYOELENAQSEGII-TLHT 962
DB 1255 TGIAFPFSSFWQORQFDIQHKGNMPCPMVLVFGCROSQKIDHIYREBTLQAKNKGVFEELYT 1314
QY 963 AFSRMPNQPTKYVQYVHWEODGKKLI--ELLDOGAHFYICGDSGMAPAVATLTKSYADV 1020
DB 1315 AYREBPDKRKYVQDILQEOQLASVYRALKQGGHIVYCGDVTMAADVLA-KIQRIMTQ 1373
QY 1021 HOVSEADARLMLQOLEEKGRYAKDV 1046
DB 1374 GKLSAEDAGVFISMARDNRYHEDIF 1399

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RESULT 10

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US-09-123-708-4
; Sequence 4, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Uergen
; APPLICANT: GODEBCKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 51169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P441402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1433
; TYPE: PRT
; ORGANISM: Cytomegalovirus
; US-09-123-708-4

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Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

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QY 457 GTPSPTEGSAKVRKKAEE-----NAHNPFLVLVYSGNMGTAGTARDLADIA 504
DB 722 GINGTPTKRRALGFKKLAEAVKESAKLMGQAMAKRVKATILVATETGSAQVAKTICEI- 780
QY 505 MSKGPAQVATLDNH-AGNLPREGAVLIVTASY-NGHPDPAKOF-----547
DB 781 FKIAFPAKVMSEBYDIHLEHETLVLVVTSTGNDPPENGKFGCALMEMHPNSVOE 840
QY 548 -----VDWLDQ-ASADEVKGVRYSVFGCGDKMATTYQKV 581
DB 841 ERKSYKVRNVSYSYDSQKSGDGPDLRNFESAGPLANRVSVGLGSR-----AYPHF 896
QY 582 PAF---IDETLAKGAENIADRGEDASDDEFTYEEMREHMSDVAAYNLT--DIENSE 636
DB 897 CAFGHAVDTLLEELGGERILKMEGDELCGQEAFTWAKVFAACDVFCVGDVNIK 956
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQPGSARST 681
DB 957 ANNSLSLNDKSMKRNKFRLLTFVAEAPLTOGLSNVHKRVSAARLSRQNLQSPKSRST 1016
QY 682 RHLEIEL--PKESAYOEGDHLGVLPRNYEGIVNRVTARFGIDA---SQQIRLEAEERK-- 734
DB 1017 IFRRLHTNGSQELQYQPGDHLGVFPGNHEDLVNALIERLE-DAPVNVQWVKELLEERN 1075
QY 735 -----LAHLPLAKTVSEELLQYVELQDPVTRTQLRAMAAKTVCPRHKELEALLE- 785
DB 1076 ALGVISNMTDELRLPCTIFQAFKYVLDITPTPTPLQLOQFASLATSSEKORLLVLSKG 1135
QY 786 KOAYKEQVLAKLRLTMLELEKYPACEMKFEFIALPSIRPRYSSISSSPRVDEKQASIT 845
DB 1136 LOEYEEKMKGNPTIYVELEEFPSIQMPATLLTQLSLQLOPRYSSISSSDMPDPDEVHLT 1195
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDITTCISTPOSEFTLPKDETPPLINWPG 904
DB 1196 VALVSVTRTRGEGEPIHHGVCSWLNRIQADELVPCFVRGAPF-FHLPRNQVPCILVPG 1254
QY 905 TGVAAPRGRVQARK-OLKEQOGSLGEANHYFGCRSPHEDVLYOELENAQSEGII-TLHT 962
DB 1255 TGIAFPFSSFWQORQFDIQHKGNMPCPMVLVFGCROSQKIDHIYREBTLQAKNKGVFEELYT 1314
QY 963 AFSRMPNQPTKYVQYVHWEODGKKLI--ELLDOGAHFYICGDSGMAPAVATLTKSYADV 1020
DB 1315 AYREBPDKRKYVQDILQEOQLASVYRALKQGGHIVYCGDVTMAADVLA-KIQRIMTQ 1373
QY 1021 HOVSEADARLMLQOLEEKGRYAKDV 1046

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Db 1374 GKLSAEDAGVFISRMDDNRYHEDIF 1399

RESULT 11

US-09-123-624-4

Sequence 4, Application US/09123624

Patent No. 6149936

GENERAL INFORMATION:

APPLICANT: SCHRAEDER, Jurgen

APPLICANT: CODECER, Axel

TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

FILE REFERENCE: 511169-2004

CURRENT APPLICATION NUMBER: US/09/123,624

PRIOR FILING DATE: 1998-07-28

PRIOR APPLICATION NUMBER: 08/553,503

PRIOR FILING DATE: 1996-03-01

PRIOR APPLICATION NUMBER: 4411402.8

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 1433

TYPE: FRT

ORGANISM: Homo sapiens

US-09-123-624-4

Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

Db 457 GIPSPSTEQSAKVKKAE-----NHNTPPLVLVYGSNMGTAGTARDLADIA 504

Db 722 GTNGPTPKRRAIGKRLAEAVKFSAKLMGQAMAKRVKATILVATETGSAVAKTLCETI- 780

Qy 505 MSKGFAPQVATLDH-AGNLPREGAVLITVASY-NGHPPDNAQOF----- 547

Db 781 FKHAFDKVMSEBYDIVHLEHETLVLVVSTFGNGDPENGEKFGCALMEMRHPNSVOE 840

Qy 548 -----VMDLQD-ASADEVKVRYSVFGCGDKNATTYQKV 581

Db 841 ERKSYKVRNFSVSSYSDQSGDGPDLRDNFESAGFLANVRSVFGLSR---AYPHF 896

Qy 582 PAF--IDETLAAGAENIADRGDASDDEGTVEERHEHMSDVAAYFNL--DIENSE 636

Db 897 CAFGHAVDTLLELGERIILKMRGSDDELCOGEBAFRTAKKAVFRAACVFCVGDVNIEX 956

Qy 637 DNKATLS-----LQVDSADNP--LAKKH--GAFSTNVVASKELQOPGASRST 681

Db 957 ANNSLISNDRSWMKRNKFRITFVAEAPBLTQGLSNVHKRVSAAARLLSRQNPSPKSRST 1016

Qy 682 RHLLEIL--PKESAYOEGDHLGVI PRNVEGIVNRYTARFGDA---SQQIRLEAEEK-- 734

Db 1017 IFVRLHNTGSOELOQOPGDHGVFPFGNHEDLVNAILERLE-DAPPVNMVVELLEERT 1075

Qy 735 -----LAHLPLAKTVSEELLQYVELQDPVTRQLRANAAKTVCPPHKELEALLE- 785

Db 1076 ALGVISNMTDELRLPPTCTFOAFKYLDITTPPRLQIQOPASLASEKQRLLVLVSKG 1135

Qy 786 KQATKEQVLAKRLMELLEKYPACEMKFSFIALPSIRRYYSISSSPRYDEKQASIT 845

Db 1136 LQEEYEMKMGKNPITVELEEFPSIQMPATLLTLQSLQPRYYSSISSPMYDPDEVALT 1195

Qy 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPDPEPTPLIMGPG 904

Db 1196 VAISYRRDDEGPIHNGVSCSWLNRIDADELVPCFVAGAPS-FLHPNPOVPCILVGPB 1254

Qy 905 TGVAFRFGVQARK-QLKEGOSLGEAHLVFGCSRHEDYLYOBELENAQSEGII--TLAT 962

Db 1255 TGIAIPFRSFWQORQDIOHKGNPCPMVLVFGCQGSKDIDHYRETTLOAKKGVFRELYT 1314

Qy 963 AFSPMPNPQKTYIVQVWEQDGKLLI--ELLQGAHFYICGDSQMAPAVETLTKMSYADV 1020

Db 1315 AYSREDPKPKYVODILOEQLAESVYRALKEOGGHIVYCGDVTMAADVLKA-IQRLMTQQ 1373

Qy 1021 HOVSEADARLMLQLEKEGRYAKDW 1046

Db 1374 GKLSAEDAGVFISRMDDNRYHEDIF 1399

RESULT 12

US-08-880-342-21

Sequence 21, Application US/08880342

Patent No. 6218179

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.

APPLICANT: Bishopric, Nanette H.

APPLICANT: Murphy, Brian

APPLICANT: Laderoute, Keith R.

APPLICANT: Green, Christopher J.

TITLE OF INVENTION: Tissue Specific Hypoxia Regulated

TITLE OF INVENTION: Therapeutic Constructs

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Delinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342

FILING DATE: 23-JUN-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996

FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486

FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 38,615

REFERENCE/DOCKET NUMBER: 8255-0018.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1433 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-880-342-21

Query Match 12.4%; Score 675; DB 4; Length 1433;

Best Local Similarity 28.0%; Pred. No. 4.9e-50;

Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

Db 457 GIPSPSTEQSAKVKKAE-----NHNTPPLVLVYGSNMGTAGTARDLADIA 504

Db 722 GTNGPTPKRRAIGKRLAEAVKFSAKLMGQAMAKRVKATILVATETGSAVAKTLCETI- 780

Qy 505 MSKGFAPQVATLDH-AGNLPREGAVLITVASY-NGHPPDNAQOF----- 547

Db 781 FKHAFDKVMSEBYDIVHLEHETLVLVVSTFGNGDPENGEKFGCALMEMRHPNSVOE 840

Qy 548 -----VMDLQD-ASADEVKVRYSVFGCGDKNATTYQKV 581

Db 841 ERKSYKVRNFSVSSYSDQSGDGPDLRDNFESAGFLANVRSVFGLSR---AYPHF 896

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QY 582 PAF---IDETLAKGAENIADRGADASDDEGTYEEMREHMSDVAAYFNL--DIENSE 636
| | | | |
DB 897 CAFGHAVDTLLEELGSRILKMRGDELCSGBAFRTWAKVFAACDVFCVGDVNIIEK 956
| | | | |
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
| | | | |
DB 957 ANNSLSINDRSWKKNKFRLLTFVABAPLTLQGLSNVHKRVSAARLBSRONLQSPKSRST 1016
| | | | |
QY 682 RHEIEL--PKESAYOEGDHLGVI PRYEGIVNVTARFGLDA---SQOIRLEAEERK-- 734
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DB 1017 IFRRLHNGSQELOYOQGDHLGVFPNGHEDLVNALIERLE-DAPPVQWAKVELLEERNT 1075
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QY 735 -----LAHLPLAKTVSVEELLQYVELODPVTROTLRMAAKTVCPPHKEVLEALLE- 785
| | | | |
DB 1076 ALGVISNWTDELRLPCTIFQAFKYLDTTPPTPLQLOQFASLATSSEKQRLVLVSKG 1135
| | | | |
QY 786 KQAYKEQVLAKRLTLMLELEKYPACEMKFSFILLISIRPRYSSISSPRVDEKQASIT 845
| | | | |
DB 1136 LOEYEEKWKGNKPTIVLEBFPSIQMPATLLTLQLSLQPRYSSISSSDMPDEVHLT 1195
| | | | |
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDETPPLINVGPG 904
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DB 1196 VALVSYTRBGEPIHHGVCSWLNRIQADELVPCFVRGAPS-FHLPRNPQVCILVGP 1254
| | | | |
QY 905 TGVAPRGRFYQARK-OLKEGOSLGEAHLVFGCRSPHEDVLYOEBELNASEGII-TLHT 962
| | | | |
DB 1255 TGLAPFRSFWQORQFDIOHKGNMPCPVLVFGCRQSKIDHLYREETLQAKNKGVFRELYT 1314
| | | | |
QY 963 AFRMPNPQPTYVOHVMEDQKLI--ELLDGAHFITCGDGSQMAPAVEATLMKSYADV 1020
| | | | |
DB 1315 AYREBPDKPKKYVDIIOEQLAESVYRALKEOGGHIYVCGDVTMAADVLA-IGRIWTOQ 1373
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QY 1021 HOVSEADARLMOOLEKGRYAKDV 1046
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DB 1374 GKLSAEDAGVFSMRDNRHYHEDIF 1399
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RESULT 13
US-08-365-486A-19
; Sequence 19, Application US/08365486A
; Patent No. 5834306
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-19

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Query Match 12.4%; Score 675; DB 2; Length 1434;
Best Local Similarity 28.0%; Pred. No. 4.9e-50;
Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

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QY 457 GIPSPTEQSAKKVRKAE-----NAHNPPLVLVYGSNMGTAGTRDLADIA 504
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| | | | |
QY 505 MSKGFAPQVATLDSH-AGNLPREGAVLITVASY-NGHPNDNAOF----- 547
| | | | |
DB 782 FKHAFDAKWSMEBYDVLVHEHETLVLVSTGNGDPRNGKFGCALMEMHNPNSVOE 841
| | | | |
QY 548 -----VDWLDQ-ASAEVKGVRYSVFGCGDKNATTYQKV 581
| | | | |
DB 842 ERKSYKVRFSVSASDSQKSGDGPDLRDNFESAGPLANVRFSVGLGSR-----AYPHF 897
| | | | |
QY 582 PAF---IDETLAKGAENIADRGADASDDEGTYEEMREHMSDVAAYFNL--DIENSE 636
| | | | |
DB 898 CAFGHAVDTLLEELGSRILKMRGDELCSGBAFRTWAKVFAACDVFCVGDVNIIEK 957
| | | | |
QY 637 DNKSTLS-----LOFVDSADMP--LAKMH--GAFSTNVVASKELQOGSARST 681
| | | | |
DB 958 ANNSLSINDRSWKKNKFRLLTFVABAPLTLQGLSNVHKRVSAARLBSRONLQSPKSRST 1017
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QY 682 RHEIEL--PKESAYOEGDHLGVI PRYEGIVNVTARFGLDA---SQOIRLEAEERK-- 734
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QY 735 -----LAHLPLAKTVSVEELLQYVELODPVTROTLRMAAKTVCPPHKEVLEALLE- 785
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DB 1077 ALGVISNWTDELRLPCTIFQAFKYLDTTPPTPLQLOQFASLATSSEKQRLVLVSKG 1136
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QY 786 KQAYKEQVLAKRLTLMLELEKYPACEMKFSFILLISIRPRYSSISSPRVDEKQASIT 845
| | | | |
DB 1137 LOEYEEKWKGNKPTIVLEBFPSIQMPATLLTLQLSLQPRYSSISSSDMPDEVHLT 1196
| | | | |
QY 846 VSVVSGEAMSGYGE-YKGIASNYLAELQEGDTITCFISTPQSEFTLPKDETPPLINVGPG 904
| | | | |
DB 1197 VALVSYTRBGEPIHHGVCSWLNRIQADELVPCFVRGAPS-FHLPRNPQVCILVGP 1255
| | | | |
QY 905 TGVAPRGRFYQARK-OLKEGOSLGEAHLVFGCRSPHEDVLYOEBELNASEGII-TLHT 962
| | | | |
DB 1256 TGLAPFRSFWQORQFDIOHKGNMPCPVLVFGCRQSKIDHLYREETLQAKNKGVFRELYT 1315
| | | | |
QY 963 AFRMPNPQPTYVOHVMEDQKLI--ELLDGAHFITCGDGSQMAPAVEATLMKSYADV 1020
| | | | |
DB 1316 AYREBPDKPKKYVDIIOEQLAESVYRALKEOGGHIYVCGDVTMAADVLA-IGRIWTOQ 1374
| | | | |
QY 1021 HOVSEADARLMOOLEKGRYAKDV 1046
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DB 1375 GKLSAEDAGVFSMRDNRHYHEDIF 1400
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RESULT 14
US-08-880-342-19
; Sequence 19, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Ladroute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates

```

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QY 457 GIPSPSTQSAKKRYKKKE-----NAHNTPLLVYXGSMWGAEGTARPLADIA 504
Dh 723 GTNGTPYTKRALIGFKKLAEAVKFSKLMGQAMAKVKATILYATITGKSQAYAKTLCI- 781
QY 505 MSKGAPQVATLDSH-AGNLPRGAVLIVTASY-NGHPDPAKOP----- 547
Dh 782 FKHAFDAKVMSEBYDIHLEHETLVLVYTSFGNGDPPENGEKFGCALMEWRHNSVOE 841
QY 548 -----VBLUDO-ASADEVKGYRYSIFGCGDKMATTYQKV 581
Dh 842 ERKSYKVFENSVSSYSDBQSKSGDGPDLRDNFESGPLANRVSVFGGSR-----AYHF 897
QY 582 PAF---IDETLAAKAENIADRGADASDDFEGTAEEMREHMSSVAAVFNL--DIENSE 636
Dh 898 CAFGHAUVTLLBELGERILTKMREDELCQGEBAARTAKVKFKAACVFCGDDVNI EK 957
QY 637 DNKSTLS-----LQPVDSAADMP-LAKNH--GAPSTNVASKEILOQPSASST 681
Dh 958 ANNSIISNDRSWKRMKFRLTFVAEAPELTQGLSNVHKKRVSAPARLSRONLQSPKSRST 1011
QY 682 RHLEEL--PREASTQOEGDHLGVITRANEGIVNRTARFGDA---SQOIRLEAEERK-- 734
Dh 1018 IFVRLLHTNGSLOLQOPGDHLGVFPGNHEDLVNALIELE-DAPVNMQVKELLEERT 1076
QY 735 -----LAHLPLAKTVSVEELLQYVELODVPVTRTOLRAMAKVCPPHKVELALLE- 785
Dh 1077 ALGVISNMNTDELRLPRCTIFQAFKYUDDITTPPTLOLQOPRSLATSEKQORLLVLSKG 1133
QY 786 KOAYKEQVLAURLTMLLELEKYPACEMKRFSEFIALPSIRPYYSISSPRVDEKQASIT 845
Dh 1137 LOEVEEMWKGNKPIVEVLEEPSIQMDATLLTLQSLLOPRYYSISSPDWYPDVXHUT 1199
QY 846 VSVVSGEAMSGYGE-YKGIASVYLALEQEGDITTFISTPQSEFLPLPDPPEFLLMVGRG 904

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05 843 EPKSVKVP

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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:06:29 ; Search time 53 Seconds
(without alignments)
2001.555 Million cell updates/sec

Title: US-10-031-241-35
Perfect score: 5457
Sequence: 1 TTKEMPQPTFGELKNLPL.....RLWLQQLLEKGRYAKDVMAG 1048

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	705.5	12.9	588	US-09-765-873A-14	Sequence 14, App1
3	675	12.4	1433	US-10-224-249-14	Sequence 14, App1
4	665.5	12.2	1144	US-09-870-759-124	Sequence 12, App1
5	650	11.9	1153	US-10-224-249-13	Sequence 13, App1
6	650	11.9	1153	US-09-992-056-2	Sequence 15, App1
7	608.5	11.2	1203	US-10-224-249-15	Sequence 15, App1
8	598	11.0	679	US-10-138-838-117	Sequence 117, App1
9	598	11.0	679	US-10-139-031-117	Sequence 117, App1
10	598	11.0	679	US-10-138-905-117	Sequence 117, App1
11	598	11.0	679	US-10-138-916-117	Sequence 117, App1
12	598	11.0	679	US-09-976-800-117	Sequence 117, App1
13	597	10.9	679	US-10-138-838-83	Sequence 83, App1
14	597	10.9	679	US-10-139-031-83	Sequence 83, App1
15	597	10.9	679	US-10-138-905-83	Sequence 83, App1
16	597	10.9	679	US-10-138-916-83	Sequence 83, App1
17	597	10.9	679	US-09-976-800-83	Sequence 83, App1
18	594	10.9	679	US-10-138-838-118	Sequence 118, App1
19	594	10.9	679	US-10-139-031-118	Sequence 118, App1

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21	594	10.9	679	9	US-10-138-916-118	Sequence 118, App
22	594	10.9	679	9	US-09-976-800-118	Sequence 118, App
23	594	10.9	679	10	US-09-911-781-11	Sequence 11, App1
24	593	10.9	679	9	US-10-138-838-84	Sequence 84, App1
25	593	10.9	679	9	US-10-139-031-84	Sequence 84, App1
26	593	10.9	679	9	US-10-138-905-84	Sequence 84, App1
27	593	10.9	679	9	US-10-138-916-84	Sequence 84, App1
28	593	10.9	679	9	US-09-976-800-84	Sequence 84, App1
29	540.5	9.9	698	9	US-09-371-347-44	Sequence 44, App1
30	534.5	9.8	698	9	US-09-371-347-2	Sequence 2, App1
31	534.5	9.8	698	9	US-09-371-347-21	Sequence 21, App1
32	534.5	9.8	698	9	US-09-371-347-42	Sequence 42, App1
33	524	9.6	697	9	US-09-371-347-46	Sequence 46, App1
34	496	9.1	597	9	US-09-778-319-2	Sequence 2, App1
35	466.5	8.5	682	9	US-09-371-347-22	Sequence 22, App1
36	420.5	7.7	524	9	US-09-992-598-264	Sequence 264, App
37	420.5	7.7	524	9	US-09-989-293A-264	Sequence 264, App
38	420.5	7.7	524	9	US-10-063-547-54	Sequence 54, App1
39	420.5	7.7	524	9	US-09-989-735-264	Sequence 264, App
40	420.5	7.7	524	9	US-09-990-444-264	Sequence 264, App
41	420.5	7.7	524	9	US-09-989-730-264	Sequence 264, App
42	420.5	7.7	524	9	US-09-990-436-264	Sequence 264, App
43	420.5	7.7	524	9	US-09-991-181-264	Sequence 264, App
44	420.5	7.7	524	9	US-09-993-687-264	Sequence 264, App
45	420.5	7.7	524	9	US-09-989-734-264	Sequence 264, App

ALIGNMENTS

RESULT 1
US-09-371-347-23
Sequence 23, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN MENTIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OR INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 677
TYPE: PRT
ORGANISM: Homo sapiens
US-09-371-347-23

Query Match 14.0%; Score 766; DB 9; Length 677;
Best Local Similarity 32.4%; Pred. No. 8, 1e-48;
Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;

QY 444 FVYKAKSKIP---LGGIPSPSTEQS-AKKVKKAKENANHTPLVLYGSMGTAGCTAR 498
DB 42 FLRKKKKEVEPTTKIQTLLTSVRESSFVEKMKKTGRN-----IIVYGSQGTAEAFAN 96
QY 499 DLADIMSKGFAQVATLDSH---AGNLPREGAVLIV--TASY-NGHPDNKKQFYDWL 551
DB 97 RLSKDHRYGMRGMSADPEEYDLADLSSPEIDNALVFCMATYGGSDPDNADQFYDWL 156
QY 552 DQASADEVGVRYSVFCGCKJKNWATYQKVPV---FIDETLAKGAKENIDRGEADASD 608
DB 157 QETDQV-DLSGVKAAVGLGNK---TYEHFNMGKYVDKRLBGLGQRIETELGSDDDGN 211
QY 609 FEGTYEWEHWHMSDVAAFYFNLDIENSEDNKSTLSIQF---VDSA---ADMEPLAKQH-- 659

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Db 212 LEEDFTWREQMPAVCEHGFVEATGSESSIRQYELVHTDIDAKVYMGEMGRKLSYEN 271
Qy 660 -----GASFTNVVASKELQOGSARSTHLEIE- PKASVQEOGDHGLVIRNVEGI 710
Db 272 QKPFDDAKNPLAAVTTIRKLNQ-GTERHLMLEBUDSDSKIRYESGDHVAVPANSGAL 330
Qy 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEBELLQYVELQDPVTRTOLPAMA 768
Db 331 VNOGKILGADLDVVMISLNNIDESNKKHPPCTSYRTALTYLDITNF-PRINVLVEL 389
Qy 769 AKTYCPHAKVELEALLE-----KQAYKEQVLAKRLTMLELEKYPACMKSEFFIALP 822
Db 390 AQVASEPSEOBLEKRMASSGEGKELYLSWVEARRHIALIQCPSPILRPDIHCEILP 449
Qy 823 SIRPRYSISSPRVDEKQASITVSVSGEAMSGVGEKGIASNYL-AELOEGDT----- 876
Db 450 RLQKRTYSISASSKVHNSVHICAVVEYETKAGRIN-KGATATMLRKKEVGVENGGRAL 508
Qy 877 ITCFISTPOSEFTLPKQDEPLINVGPGTVAPRFGVQARKOLKEQOSLGEAHLTFGC 936
Db 509 VPMFVR--KSGFRLPFAKTFVIMVGPETGVAPIGFIQERAMLRQOGKEVGETLLVYGC 566
Qy 937 RSPHEDYLYOEBLENAOSEGIIT-LHTAFSMPNOPKTYVOHVEODSKULIELLDQAH 995
Db 567 RRSDELYLYREBLAQPHRDGALTQLNVAFSREOSH-KYVVOHLKODREHLMKULIEGGAH 625
Qy 996 FYICGDSQMAPAYEATLMKSYADVHOVSEADARLMLQOLEBKGRYAKDWA 1047
Db 626 IYVCGDARNMARDVONTTYDIALVAGELMEHAQAVDIKMTKGRYSLDWS 677

```

RESULT 2

```

US-09-765-873A-14
: Sequence 14, Application US/09765873A
: Patent No. US20010053847A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Xiao-Song
: TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
: FILE REFERENCE: BC1009 US CIP
: CURRENT APPLICATION NUMBER: US/09/765,873A
: CURRENT FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: US 09/627,216
: PRIOR FILING DATE: 2000-07-27
: PRIOR APPLICATION NUMBER: US 60/147,719
: PRIOR FILING DATE: 1999-08-06
: NUMBER OF SEQ ID NOS: 38
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 14
: LENGTH: 588
: TYPE: PRT
: ORGANISM: Helianthus tuberosus
US-09-765-873A-14

```

Query Match 12.9%; Score 705.5; DB 10; Length 588;
 Best Local Similarity 31.9%; Pred. No. 1.8e-43;
 Matches 189; Conservative 92; Mismatches 245; Indels 67; Gaps 19;

```

Qy 499 DLADIAMSKGPAQVATLDSHAGNLPREGAVLITVASY-NGHPPDNMKQFVMDLQASAD 557
Db 18 DLDDIYA-----ADDEEYAEKFKKETFAPFLATYGDEPTDNARFKMTLEG-- 65
Qy 558 EVKGV-----RYSVFGCGDKRMATTYQVPAFIDETLLAKAENIADRGADASDDEFGT 612
Db 66 DDKVWVLEKHYGVFGNGKQY-EHFNKIALVNBEGULQEGAKRFVPVGLGDDDDOSIEDD 124
Qy 613 YEEPREHMSDVAAVFNIDINSEDNKS-----TISL-----QFVSAADMPL 655
Db 125 FSAKKEIWPBELLDL-LD-----EDDKTAATPYTAALPEYRVVFDKXDPFSEHNSQTNG 179
Qy 656 AKMGGA---FSTNVVASKELQOGSARSTRLEIELEPKA-SYOGDHLGVIPIPNYEGIV 711
Db 180 HTVDAHQPCRSNVAVKELHTPESDRSCHLEPDISHTGSLYETGDDHVGVCENLIEIV 239

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Qy 712 NRYTARFGLDASQOIRLEAEBEKLAHL-----PLAKTVSEBELLQYVELQDPVTRTOL 764
Db 240 EBAEKILGLPADYVPSLHIDNEDGTPLGPTLPPEPPCTLRALNTVADLLSPKKSTL 299
Qy 765 RAMAAKTVCPHAKVELEALLE---KQAYKEQVLAKRLTMLELEKYPACMKSEFFIAL 820
Db 300 LAAAHASDYTEADRLQFLASREGKDEYEMIVANORSLEVEAREPPSAKPLGVFFPAAI 359
Qy 821 LPSIRPRYSISSPRVDEKQASITVSVSGEAMSGVGEKGIASNYL-----LAELOEG 874
Db 360 APRQEPRTYSISSPKPVNPRHIVTCALY-EXTPGRIHKGICSTMKKAIVPLTEHQDC 418
Qy 875 DITTCFISTPOSEFTLPKQDEPLINVGPGTVAPRFGVQARKOLKEQOSLGEAHLTF 934
Db 419 SSAPIFVRT--SNFRLPADPKVPMIGPBTGLAPRFGFIQERLALKESTELGQSTLFF 476
Qy 935 GCSPHEDYLYOEBLENAOSEGIIT-LHTAFSMPNOPKTYVOHVEODSKULIELLDQ 993
Db 477 GCNRKVDFTYERELNNFENGALSELDMVFSR-EGASKERYVOHKMSQKASDIMMLSEG 535
Qy 994 AHFYICGDSQMAPAYEATLMKSYADVHOVSEADARLMLQOLEBKGRYAKDWA 1046
Db 536 AYLYVCGDARKMAKDVRHTLHTTVQEGNLDSSKALYVKNLQMSGRYLRDW 588

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RESULT 3

```

US-10-224-249-14
: Sequence 14, Application US/10224249
: Publication No. US20030087867A1
: GENERAL INFORMATION:
: APPLICANT: Vogels, Ronald V.
: TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis
: FILE REFERENCE: 2183-5233US
: CURRENT APPLICATION NUMBER: US/10/224,249
: CURRENT FILING DATE: 2002-08-19
: PRIOR APPLICATION NUMBER: PCT/NL00/00482
: PRIOR FILING DATE: 2000-07-07
: PRIOR APPLICATION NUMBER: EP 99202263.2
: PRIOR FILING DATE: 1999-07-09
: PRIOR APPLICATION NUMBER: US 60/143,101
: PRIOR FILING DATE: 1999-07-09
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 14
: LENGTH: 1433
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CHAIN
: LOCATION: (1)..(1433)
: OTHER INFORMATION: Human nitric oxide synthase
US-10-224-249-14

```

Query Match 12.4%; Score 675; DB 9; Length 1433;
 Best Local Similarity 28.0%; Pred. No. 1.2e-40;
 Matches 192; Conservative 132; Mismatches 258; Indels 104; Gaps 23;

```

Qy 457 GTPSPTEGSAKVKRKAAE-----NAHNTPLVLVYSGNMGTACTGARDLADIA 504
Db 722 GTNGTPPKRAAIFKKLAIEVKSAKLMGQAMKRVYATLLVATETGKSAVAKTICEI 780
Qy 505 MSKGAPQAVATLDSH-AGNLPREGAVLITVASY-NGHPPDNMAKOF----- 547
Db 781 FKXAFDAKVMSEEDYIVLHEHETLVAVTSTGNGDPPNNGEKFGCALMEMHNSVOE 840
Qy 548 -----VDWLDQ-ASADEVKGVRSVFGCGDKRMATTYQV 581
Db 841 ERKSYKVRFNVSYSQSGDGPDLRNPFSAAGPLAVRFSVFGLSR-----AVPHF 896
Qy 582 PAF---IDETLLAKAENIADRGADASDDEFGTEYEMRHHMSDVAAVYNTL--DIENSE 636
Db 897 CAFGHAVDTLLEBLGGERILMKREGDELQGEAEAFRTMAKVKVKAACDVFCVDDVNIK 956

```


Db 613 KELNNK-FRYAVFGLG-----SSMYPRFCAFAHDIDOKLSHLGASQLTLMGEGDELSCQED 667

Qy 612 TYEEMREHMMS-----DVAAYFNLDIENSEDNKSTLS---LQPVDSADMPPLAK-----M 658

Db 668 AFRSMNAVOTFKAACETFDVGRGKHIOI PKLYTSNVTMDPHHYRLVODSOPLDLSKALSSM 727

Qy 659 H--GAFSTNVVASKELQOPGSARSTRHLEI--ELPKASYOEGDHLGVIPRNYEGIVNRV 714

Db 728 HAKVFTMRKSRQNLQSPSTSSRATILVELSCEDGQGLNLPBHLGVCPGNQALVQGI 787

Qy 715 TARF--GLDASQOIRLEAEKEKLAHLPLAKTV--SVEELLOY-VELODPVTRTOLRAMA 768

Db 788 LERVVDGPTPHQVTRLLEDLDESGSYWSDKRLPPCSLSQALTVSPDITPTPTOLLQKLA 847

Qy 769 AKTVCPRHKVELLEALKQAYKEQVLAKRLTMLELEKYPACEMKSEFIALLPISIRPY 828

Db 848 QVATEEBERQRLBALCPSEYSKMKFTNSPTFLEVEEFSLVRSAGLSQILKPRF 907

Qy 829 YSISSSPRVDEKQASITVSVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPQSE 887

Db 908 YSISSSRDHPTPEIHLTVAVVTYHTGDGQGPLHHGVCSWTLSLKPDQPVPCFVRN-ASA 966

Qy 888 FTLPKDETPILMVGPGTGVAPFRGFOVAR-KOLKEGQSLGEAHLTFGCRSPHEDLYQ 946

Db 967 FHLPEDPSHPCLILGPGTGIVPFRSFWOQRLHDSQHKVGRGRTLVFGCRRPDEDHLYQ 1026

Qy 947 EE-LENQSEGITLHTAFSRMPNQPRTYVOHWMED--GKKLIELDQGAHFYICGDS 1003

Db 1027 EEMLEMAQKGLVAHVHTAYSRLPGKPKRYVODITLRQOLASEVLRVHLKHEPCHLYVCGD-V 1085

Qy 1004 QMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGARYADW 1046

Db 1086 RMRADVHTLKQLVAALKKLINEQVEDYFQLKSQKRYHEDIF 1128

RESULT 6

US-09-992-056-2

Sequence 2, Application US/09992056

Patent No. US20020061862A1

GENERAL INFORMATION:

APPLICANT: Billiar, Timothy R.

APPLICANT: Tzeng, Edith

APPLICANT: Nussler, Andreas K.

APPLICANT: Geller, David A.

APPLICANT: Simmons, Richard K.

APPLICANT: Shears II, Larry L.

TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of

TITLE OF INVENTION: Disease

FILE REFERENCE: 213298

CURRENT APPLICATION NUMBER: US/09/992, 056

CURRENT FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: 09/176,496

PRIOR FILING DATE: 1998-10-21

PRIOR APPLICATION NUMBER: 08/465,522

PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: 08/314,917

PRIOR FILING DATE: 1994-09-28

PRIOR APPLICATION NUMBER: 07/981,344

PRIOR FILING DATE: 1992-11-25

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 1153

TYPE: PRT

ORGANISM: Induced Human Hepatocyte RNA

US-09-992-056-2

Query Match 11.9%; Score 650; DB 10; Length 1153;

Best Local Similarity 30.3%; Pred. No. 5.9e-39;

Matches 195; Conservative 112; Mismatches 272; Indels 64; Gaps 22;

Qy 447 KAKSKKIPGLGIPSPSTQSAKKYRKKA-----ENAHNTPLVLVYSSNMGTAECT 496

Db 507 RPKRREIPL-----KVLKVAVLFACMLMRKTMASERVVITLIFATETGSEAL 553

Qy 497 ARDLADIAMSGKAPAVATLDSH-AGNLPRGAVLITYTASY-NGHPDNKAKQFVMDLQ 554

Db 554 AMDLGL-ESCANPKVYCMCKYRLSCLEBERLLVVTSTFGNGDGRNGEKLSIFML 612

Qy 555 SADEVKVRYSVFCGCDKMMATTYQKVPF--IDETLAKGAENIADRGEADASDFEG 611

Db 613 KELNNK-FRYAVFGLG-----SSMYPRFCAFAHDIDOKLSHLGASQLTLMGEGDELSCQED 667

Qy 612 TYEEMREHMMS-----DVAAYFNLDIENSEDNKSTLS---LQPVDSADMPPLAK-----M 658

Db 668 AFRSMNAVOTFKAACETFDVGRGKHIOI PKLYTSNVTMDPHHYRLVODSOPLDLSKALSSM 727

Qy 659 H--GAFSTNVVASKELQOPGSARSTRHLEI--ELPKASYOEGDHLGVIPRNYEGIVNRV 714

Db 728 HAKVFTMRKSRQNLQSPSTSSRATILVELSCEDGQGLNLPBHLGVCPGNQALVQGI 787

Qy 715 TARF--GLDASQOIRLEAEKEKLAHLPLAKTV--SVEELLOY-VELODPVTRTOLRAMA 768

Db 788 LERVVDGPTPHQVTRLLEDLDESGSYWSDKRLPPCSLSQALTVSPDITPTPTOLLQKLA 847

Qy 769 AKTVCPRHKVELLEALKQAYKEQVLAKRLTMLELEKYPACEMKSEFIALLPISIRPY 828

Db 848 QVATEEBERQRLBALCPSEYSKMKFTNSPTFLEVEEFSLVRSAGLSQILKPRF 907

Qy 829 YSISSSPRVDEKQASITVSVSGEAMSGYGE-YKGIASNYLAELQEGDITTCFISTPQSE 887

Db 908 YSISSSRDHPTPEIHLTVAVVTYHTGDGQGPLHHGVCSWTLSLKPDQPVPCFVRN-ASA 966

Qy 888 FTLPKDETPILMVGPGTGVAPFRGFOVAR-KOLKEGQSLGEAHLTFGCRSPHEDLYQ 946

Db 967 FHLPEDPSHPCLILGPGTGIVPFRSFWOQRLHDSQHKVGRGRTLVFGCRRPDEDHLYQ 1026

Qy 947 EE-LENQSEGITLHTAFSRMPNQPRTYVOHWMED--GKKLIELDQGAHFYICGDS 1003

Db 1027 EEMLEMAQKGLVAHVHTAYSRLPGKPKRYVODITLRQOLASEVLRVHLKHEPCHLYVCGD-V 1085

Qy 1004 QMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGARYADW 1046

Db 1086 RMRADVHTLKQLVAALKKLINEQVEDYFQLKSQKRYHEDIF 1128

RESULT 7

US-10-224-249-15

Sequence 15, Application US/10224249

Publication No. US20030087867A1

GENERAL INFORMATION:

APPLICANT: Vogels, Ronald V.

APPLICANT: Verlinden, Stefan F.F.

TITLE OF INVENTION: Gene therapy for enhancing and/or inducing angiogenesis

FILE REFERENCE: 2183-5233US

CURRENT APPLICATION NUMBER: US/10/224, 249

CURRENT FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: PCT/NL00/00482

PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: EP 99202263.2

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: US 60/143,101

PRIOR FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15

LENGTH: 1203

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CHAIN

LOCATION: (1) (1203)

OTHER INFORMATION: Human nitric oxide synthase

US-10-224-249-15

Query Match 11.2%; Score 608.5; DB 9; Length 1203;

Best Local Similarity 26.7%; Pred. No. 7e-36;
Matches 191; Conservative 115; Mismatches 254; Indels 155; Gaps 24;

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QY 454 PLGGISPSPEQSAKKYRKAEN-----AHNPLVLIVGSMNGTEGARDL 500
Db 479 PMKGSAAKGGITRRKTFKAVANA VKISASLMGTWAKRKYATLLVGETGRQSYAQQ 538
QY 501 ADIAMS KGAPOVATLDSH--AGNLPRGAVLITVASY--NGHPPDNAKQFV-----548
Db 539 GRV--FKAPDPRVLCMDYVVLHEHTLVLTSTFGNDPDPENGSSFAALAMENSGPY 597
QY 549 -----DW-----LDQASADEVKGVRYSVFCCGDKW 574
Db 598 NSSPREOHSKYKIRFNSISCDPLVSWRRKRKESSENTDSAGALTFRFCVGLGSR-- 655
QY 575 ATTYQVPAF---IDETLAAGAENIADRGADASDFEGTYEEMRHMSDVAAAFNLD 631
Db 656 --AHPHCAFAVADTRLEELGGERLQLQGGDELCCQEBAFRGMAQAAQAAACETFCV- 712
QY 632 IENSEDNKSTL-----SLQFVDSAADMPILAKMHGAFSTNVVAS 669
Db 713 ---GDAKAAARDIFSPKRSWKQRVRLSAQABGLQLPLGLIHVRKM---FOATIRSV 766
QY 670 KELQPGASRSTRHLEIEL--PKASYQESDHLGVI PRNYEGIVNRYTARFGLDASQQR 727
Db 767 ENLQSKSTRATILVRLDTGQGGELQYQPGDHLGVCPNRPGLVEALLSR-----816
QY 728 LEAEERKLAHLPLAKT--VSVEELQ-----YVELQDP 758
Db 817 --VED-----PAPPEPAVEQLEKSGPGCPPGVNRDLRPPCTLRQALTFLDTSP 868
QY 759 VTRTOLRAMAKTVCPPHKVELEAL--LEKQAYKEQVLAKRLTMLELEKRPACEMKFSF 817
Db 869 PSQQLRLSTLAEEPREQOELEALSODPRRYEEMKFRCPITLLEVLCQPSVALPRL 928
QY 818 IALLPSIRPRYYSISSSPRVDEKQASITVSVSGEAMSGYGE--YKGIASVYLAELQEDT 876
Db 929 LTQLPLQPRYVSVAFTSTHPEIHLTVAVLAVRTQDGLGPLHYGCVSTWLSQLKPGDP 988
QY 877 ITCEFTPQSEFTLPDPETPLIMGPGCTGVARPRGVQAR--KQKQSGSLGSAHLVYG 935
Db 989 VPFILGAPR--FLPDPSPSLPCILVGGTGIAPRGWQERLHDIKSGLOPTPMTLVFG 1047
QY 936 CRSPHEDVLYQOELENAQSEGI--TLHTASRMPNOPTVVOHMEQDGKKLIE---LLD 991
Db 1048 CRSQDLHLRYDEVQAQGVGRVLTASRBDNKTIVQDILRLELAEVAHRVLCLE 1107
QY 992 QGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLQOLEEKGRYAKDVW 1046
Db 1108 RG-HMEVCCDVT--MATVVLQTVQRIATLGEDEMEDEAGDIVIGVLRDQORYHEDIF 1160

```

RESULT 8

US-10-138-838-117
Sequence 117, Application US/10138838
Publication No. US20030049821A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eschoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10138, 838

CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976, 800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 117
LENGTH: 679
TYPE: PRT
ORGANISM: CANDIDATROPICALIS
US-10-138-838-117

Query Match 11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

```

QY 430 ELDIKETLLKPEGFFVAKSKKI-----PLGGIPSTQSAKKYRKAENAHNTLLVL 485
Db 5 KLDLVYITLVVAVAAYFAKNQFLDQPDQTFPLNTDSGNSRDLSTLKKNNNT--LTL 62
QY 486 YGSNMGTAGTARDLADIAMSK--GFAPQVATLDSH-----AGNLPRGAVLITVASY--NGH 539
Db 63 FSGQTATADYANKLSRELHSRGLKTMVADPADYDMNFGDITIEDILVFFIATYGBGE 122
QY 540 PRDNARQPVDMIDQASADEVKGVRYSVFCGDKNMATYQKVPF---IDETLAAGAEN 596
Db 123 PTDNADEFHTWLTE--BADTLSTLKYTVFGLGN---STVEFNAIGRKFDRLSEKGD 177
QY 597 IADRGADASDDEPGYEE--WRHMSDVAAAFNLD-----631
Db 178 FAEYAE--GDDGTGLDEDFMAKNVNDALKNIDFEEKELKYPNVKLTERRDLSAA 234
QY 632 ---IENSEDNKSTLSLQFVDSAADMPILAKMHGAFSTNVVASKELQPGASRSTRHLEIEL 688
Db 235 DSGVSLGEENKKYINBEGIDLTVG--PFDRTH--PYLARITETRLFS--SKDRHCHIVEFDI 291
QY 689 PK-EASYQEGDHLGVI PRNYEGIVNRYTARFGLDASQQRILEAE--EKLAHLPLAKTVSV 746
Db 292 SESNLKTYTGDLHAIWPSNSDENIKQFACFGLEDLDTVIELEKADSYTYTIPFPITY 351
QY 747 BELLO--YVLEODPVTRTOLRAMAKTVCPPHKVELEAL---EKQAYKEQVLAKRLTML 801
Db 352 GAVIRHHLISGVSSQFSLISG---FAPDETKAFTRLGDKQEFPAKVTRRKFNIA 408
QY 802 ELL---EKYPACEMKFSFIALPISIRPRYYSISSPRVDEKQASITVSVSGEAMSGY 857
Db 409 DALYSSNNAFSDVFEFLIENVPHLTRIYYSISS--SLSEQLINVTAVAEAEADG 467
QY 858 GEYKGIASVYLAELQ-----EGDTITCFISTP-----OSEFTLPKDPET 896
Db 468 RPYTGAVTMLKNAEIVQKGTGEKPLVHYDLSGPRGKFNKFLPVHRRSNFGLPKNSTT 527
QY 897 PLIMVGPGTVAPFRFQVQARQKQKQSGSLGSAHLVYFCGRSPHEHYLYQEE--LENAQSE 955
Db 528 PVLILGPGTVAPFRFQVQARQKQKQSGSLGSAHLVYFCGRSPHEHYLYQEE--LENAQSE 957
QY 956 G-IITHTAFSRMPNOPTVVOHMEQDGKKLIELDQGAHFYICGDSQMAPAVEATLM 1014
Db 588 GENFEMFNAFNRQDPKQKTYVQDKILENSQVLHELTBEAIIYVCGDASRMARDVQTTIS 647
QY 1015 KSYADVHQVSEADARLMLQOLEEKGRYAKDVW 1046
Db 648 KIVAKSREISDEKAEVLVSMKQVQNNRYQEDVW 679

```

RESULT 9

US-10-139-031-117
Sequence 117, Application US/10139031
Publication No. US20030049822A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eschoo, Mark

APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.
 APPLICANT: Tang, Maria A.
 APPLICANT: Loper, John C.
 APPLICANT: Gleeson, Martin
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 TITLE OF INVENTION: P450 OXIDOREDUCTASE
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
 FILE REFERENCE: 1010-16
 CURRENT APPLICATION NUMBER: US/10/139,031
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US/09/976,800
 PRIOR FILING DATE: 2001-10-12
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 117
 LENGTH: 679
 TYPE: PRT
 ORGANISM: CANDIDATROPICALIS
 US-10-139-031-117

Query Match 11.0%; Score 598; DB 9; Length 679;
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

430 ELDIKELTLLKPGFVAVAKSKI-----PLGGIPSPTEOSAKVKRKAENHTPLVL 485
 5 KLDYVITITLVAVAAVAFKQFLDQPODTGFLNTDSGNSRDVLTSLKKNKNT--LL 62
 486 YGSNMGTAEGTARDLADIAMSK-GFAPQVATLDSH---AGNLPREGAVLIVTASY-NGH 539
 63 FGSQGTGAEDYANKLSRELHSRFGKTMVADPADYDMNDGIDITEDILVFIVATYGE 122
 540 PPDKAQFVWMLDQASADEVKGVRYSGCGDKMATTYQKVPF--IDETLAKEAEN 596
 123 PTDNADEFHTLTE-EADTLSTLKYTVFGLGN---STYEFNAIGRKFRLLSEKGGDR 177
 597 IADGEADASDDFEGTVEE---WREHMSDVAAVFNLD----- 631
 178 FAETAE---GDDGTGTLDEDFPMKNDVFDALKNDLNEEKELKYEPNVKLTERRDLSAA 234
 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFTNVVASKELQOPGSARSTRHLEIEL 688
 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARTETRELFS-SKORHCIVHVEDI 291
 689 PK-EASTQEGDHCVIRNTEGIVNRVTARFGDASQOIRLEABE-EKLAHLPLAKTVSV 746
 292 SESNLYKTTGDHLAIWPSNSDENIKQPAKCFGLDKLDTVIELKALDSTYTIPEPTPTY 351
 747 EELLQ-VELODPYTRQLRAMAKTVCPRHKVELLALL---EKOAYKEQVLAARLML 801
 352 GAVIRHHLIEISGVSROFPLSIAG--FAPDEETKKAFTLGGDKQEFAPAAVTRKKNIA 408
 802 ELL-----EKYPACEMKSEFIALPSIRPRYSISSSPRVDEKQASITVSVSGEANSY 857
 409 DALIYSSNNAWSDVPEFLEINPHLTPRYTSSSS-SLSEKQIINTAVAVEABEADG 467
 858 GEYGIASNYLAELO-----EGDTTCFISTP-----QSEFTLPKDEPT 896
 468 RPYGVGVNLLKNEVEIVONKTGEKPLVHYDLSGPRGKFNKRLPVHVRNSFKLPIKSTT 527
 897 PLIIVGPGTGAVPFPGVQARKOLKEQOSLGEAHLVYGCSPHEDVLYORE-LENAQSE 955
 528 PVLILGPGTGAAPLRGFRERVOQVKNGVNKGKTLFPGCKNSNEDFLYKQEMAEYASVL 587
 956 G-IITLTAFSRMPNQPKTYVOHVMEDQKLIIEILDQAHFYICGDSQMAPAVEATIM 1014
 588 GENEMFAPAFSRQPSKVVYQDKILENSQVLHLLTGALIIYVCGDASRNARVDQTTIS 647
 1015 KSYADVHOVSADARLMLQOLEEKGRYAKDV 1046

Db 648 KIVAKSEISEDKAAELVSKWQVONRYQEDVW 679

RESULT 10
 US-10-138-905-117

Sequence 117, Application US/10138905
 Publication No. US20030068800A1

GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
 APPLICANT: Craft, David L.
 APPLICANT: Birch, Dudley
 APPLICANT: Eshoo, Mark
 APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.
 APPLICANT: Tang, Maria
 APPLICANT: Loper, John C.
 APPLICANT: Gleeson, Martin

TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 TITLE OF INVENTION: P450 OXIDOREDUCTASE
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
 FILE REFERENCE: 1010-16
 CURRENT APPLICATION NUMBER: US/10/138,905
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US/09/976,800
 PRIOR FILING DATE: 2001-10-12
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 117
 LENGTH: 679
 TYPE: PRT
 ORGANISM: CANDIDATROPICALIS
 US-10-138-905-117

Query Match 11.0%; Score 598; DB 9; Length 679;
 Best Local Similarity 27.2%; Pred. No. 1.8e-35;
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

430 ELDIKELTLLKPGFVAVAKSKI-----PLGGIPSPTEOSAKVKRKAENHTPLVL 485
 5 KLDYVITITLVAVAAVAFKQFLDQPODTGFLNTDSGNSRDVLTSLKKNKNT--LL 62
 486 YGSNMGTAEGTARDLADIAMSK-GFAPQVATLDSH---AGNLPREGAVLIVTASY-NGH 539
 63 FGSQGTGAEDYANKLSRELHSRFGKTMVADPADYDMNDGIDITEDILVFIVATYGE 122
 540 PPDKAQFVWMLDQASADEVKGVRYSGCGDKMATTYQKVPF--IDETLAKEAEN 596
 123 PTDNADEFHTLTE-EADTLSTLKYTVFGLGN---STYEFNAIGRKFRLLSEKGGDR 177
 597 IADGEADASDDFEGTVEE---WREHMSDVAAVFNLD----- 631
 178 FAETAE---GDDGTGTLDEDFPMKNDVFDALKNDLNEEKELKYEPNVKLTERRDLSAA 234
 632 ---IENSDNKSTLSLOFVDSADMPPLAKMGAFTNVVASKELQOPGSARSTRHLEIEL 688
 235 DSQVSLGEPNKKYINSEGDILTKG-PEDHTH-PYLARTETRELFS-SKORHCIVHVEDI 291
 689 PK-EASTQEGDHCVIRNTEGIVNRVTARFGDASQOIRLEABE-EKLAHLPLAKTVSV 746
 292 SESNLYKTTGDHLAIWPSNSDENIKQPAKCFGLDKLDTVIELKALDSTYTIPEPTPTY 351
 747 EELLQ-VELODPYTRQLRAMAKTVCPRHKVELLALL---EKOAYKEQVLAARLML 801
 352 GAVIRHHLIEISGVSROFPLSIAG--FAPDEETKKAFTLGGDKQEFAPAAVTRKKNIA 408
 802 ELL-----EKYPACEMKSEFIALPSIRPRYSISSSPRVDEKQASITVSVSGEANSY 857
 409 DALIYSSNNAWSDVPEFLEINPHLTPRYTSSSS-SLSEKQIINTAVAVEABEADG 467
 858 GEYGIASNYLAELO-----EGDTTCFISTP-----QSEFTLPKDEPT 896


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Db      468 RPTVGVTVNLLKKNVEIVQNTGKELVHYDLSGPRGKFNKFLPVHVRSGNFKLPKNSTT 527
Qy      897 PLIMVPGTGVAPFRGTVQARKOLKEQOSLGEAHLYFGCRSPHEDLYOEE-LENAOSE 955
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      528 PVLIGGTGVAPLRGVRRVQVQVGVNGVKTLLFYCGRNSNEDFLYQENAEYASVL 587
Qy      956 G-IITLHTAFSRMNPQKTYVQVHMEODGKKLIELLDQGAHFYICGDSGOMAPAVEATLM 1014
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      588 GENFEMFNARSRODPSKVVYVQDKLIENSQVHLLTEGAIIYVCGDASMARADVQTTIS 647
Qy      1015 KSYADVHGVSEADARLMLQOLEEKGRYAXDWM 1046
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      648 KIVAKSREISEDKAELVSKMVKVQNRQYQEDWM 679

```

```

RESULT 11
US-10-138-916-117
; Sequence 117, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138, 916
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/976, 800
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/302, 602
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-10-138-916-117

```

```

Query Match      11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

```

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Qy      430 ELDIKELTLTKPFGFVVKAKSKII-----PLGGIPSPSTEGSAKKVRKKAENANTPLVLV 485
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      5- KDLVYIITLVVAVAAYFAKNQFLDQPDQDTGFLNTDSGNSRDLSTLTKKNNKT--LLL 62
Qy      486 YGSNMGTAEGTADLADIAMS-K-GFAPQVATLDSH-----AGNLPREGAVLIVTASY-NGH 539
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 FGSQGTAEVDYANKLSRELHSRGLKTMVADPADYDMDNFGDITEDILVFFIATYGEGE 122
Qy      540 PPDNAQFVDMLDQASADEVKGRVSYFGCGDKMAATTYQKPAF---IDETLAAGAEN 596
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 PTDNADFEHTWLT-EADTLSTLKYTVFGIGN-----STYEFNNAIGKFPRLSEKGGDR 177
Qy      597 IARGGEADADDPFGTYEE---WREHMSDVAAVFLD----- 631
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      178 FAAYAE---GDDGTGLTDEDFMAKNDVFDALKNLDLFEKEKLYEBNVLTTERDLSAA 234
Qy      632 ---IENSDEKSTLSLOFVDSADMPPLAKMNGAFSTNVVASKELQCGASRSTRHLETEL 688
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      235 DSGVSLGEPRKXKYYNSGIDLTGK-PEDRTH-PLIAITETREHFS-SKRHRCHVFEFDI 291
Qy      689 PK-EASYQEGDHLGVI-PRNVEGIIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746

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Db      292 SESNLKTYTGDLHAIWPSNDSENIKQFAKCFGLKDLDTVIELKALDSTYITPPTITY 351
Qy      747 BELLQ-VYELQDPVTQTOLRAMAKATVCPPHKLEALL-----EKQAYKEQVLAKLITML 801
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      352 GAVIRHRLTSGVSRQFELIAG---FAPDETKKAFTRLGDKQKQFAKVRKRNENA 408
Qy      802 ELI-----EKYPACEMFSEPIALLPSIRPRYSISSPRVDEQASITVSGEAMSGY 857
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      409 DALLYSNNAQWSDVFEFLIENVPHLTRYYSISS-SISEQOLNVAVVAEEDADG 467
Qy      858 GEYKIASNYLAELQ-----EGDTITCFISRP-----OSEFTLPKDPET 896
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      468 RPTVGVTVNLLKKNVEIVQNTGKELVHYDLSGPRGKFNKFLPVHVRSGNFKLPKNSTT 527
Qy      897 PLIMVPGTGVAPFRGTVQARKOLKEQOSLGEAHLYFGCRSPHEDLYOEE-LENAOSE 955
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      528 PVLIGGTGVAPLRGVRRVQVQVGVNGVKTLLFYCGRNSNEDFLYQENAEYASVL 587
Qy      956 G-IITLHTAFSRMNPQKTYVQVHMEODGKKLIELLDQGAHFYICGDSGOMAPAVEATLM 1014
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      588 GENFEMFNARSRODPSKVVYVQDKLIENSQVHLLTEGAIIYVCGDASMARADVQTTIS 647
Qy      1015 KSYADVHGVSEADARLMLQOLEEKGRYAXDWM 1046
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      648 KIVAKSREISEDKAELVSKMVKVQNRQYQEDWM 679

```

```

RESULT 12
US-09-976-800-117
; Sequence 117, Application US/09976800
; Publication No. US20030077795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976, 800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 117
; LENGTH: 679
; TYPE: PRT
; ORGANISM: CANDIDATROPICALIS
US-09-976-800-117

```

```

Query Match      11.0%; Score 598; DB 9; Length 679;
Best Local Similarity 27.2%; Pred. No. 1.8e-35;
Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

```

```

Qy      430 ELDIKELTLTKPFGFVVKAKSKII-----PLGGIPSPSTEGSAKKVRKKAENANTPLVLV 485
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      5 KDLVYIITLVVAVAAYFAKNQFLDQPDQDTGFLNTDSGNSRDLSTLTKKNNKT--LLL 62
Qy      486 YGSNMGTAEGTADLADIAMS-K-GFAPQVATLDSH-----AGNLPREGAVLIVTASY-NGH 539
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 FGSQGTAEVDYANKLSRELHSRGLKTMVADPADYDMDNFGDITEDILVFFIATYGEGE 122
Qy      540 PPDNAQFVDMLDQASADEVKGRVSYFGCGDKMAATTYQKPAF---IDETLAAGAEN 596
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      123 PTDNADFEHTWLT-EADTLSTLKYTVFGIGN-----STYEFNNAIGKFPRLSEKGGDR 177

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QY 597 IADRGADASDDFEGTVEE---WREHMSDVAAYFNLD----- 631
 DB 178 FAFAE---GDDGTGLDDEDFAMKDNVFDALKNDFEELKYEPRVUKLTERDLSAA 234
 QY 632 ---IENSEDKSTLSLOFVDSADMPPLAKMHGAFSTNVVASKELQOPGASRSTRHLEL 688
 DB 235 DSQVSLGEPNKKYINSEGDILTCKG-PFDHTh-PYLARITETRELFS-SKDRHCIHVEFDI 291
 QY 669 PK-EASYOEGDHLVIRPNVEGINRVATARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746
 DB 292 SESNLKTTTGDHLAIWPSNDENIKOPAKCFGLDKLDTVLELALDSTYTPPTPTTY 351
 QY 747 EELQO-YVELQDPTVTRTOLRAMAAKTVCPRHKELEALL---EKOAYKEQVLAKRLTML 801
 DB 352 GAVIRHHLIEISGRVSRQFFLSIAG---FAPDETKKAFTRLGSGKQEPAAVTRKRNIA 408
 QY 802 ELL---EKYPACEMKFESEFIALPISIRPRYISISSPRVDEKQASITVSVSGEAMSGY 857
 DB 409 DALYSSNNAPWSVDFEFLIENVPHLTPRYISISS-SLSEKQILNVTAVVAEEADG 467
 QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----QSEFTLPKDPET 896
 DB 468 RPYTGVTNLLKNAVEIYONKTGEKPLVHYDLSGPRKFNKFLPVHVRNSFPLPKNSTT 527
 QY 897 PLIMVGPCTGVAAPRFGVQARQKQKQOSLGEAHLVFGCRSPHEDVLYQEE-LENAOSE 955
 DB 528 PVLIGPGTGVAPLRGFRERVOQVKNGVNKTLLFYGCGRNSNEDFLYKQEMAEVASYL 587
 QY 956 G-IITLHTAFSRMPNQPTTYQVHMEDQKLELIDOGAHFYICGDSGMAVAEATLM 1014
 DB 588 GENFEMFAPSRDPSKRVYVODKILENSQLVHLELLEGALIIYCGDASMRADVOJTIS 647
 QY 1015 KSYADVHOVSEADARLMLQOLEEKGRAVDW 1046
 DB 648 KIYAKSREISEDKAELVYKWKVQNRVQEDW 679

RESULT 13 US-10-138-838-83

Sequence 83, Application US/10138838
 Publication No. US20030049822A1
 GENERAL INFORMATION:
 APPLICANT: Wilson, Ron C.
 APPLICANT: Craft, David L.
 APPLICANT: Birch, Dudley
 APPLICANT: Eshoo, Mark
 APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.
 APPLICANT: Tang, Maria
 APPLICANT: Loper, John C.
 APPLICANT: Gleeson, Martin
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 TITLE OF INVENTION: P450 OXIDOREDUCTASE
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
 FILE REFERENCE: 1010-16
 CURRENT APPLICATION NUMBER: US/10/138,838
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US/09/976,800
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 83
 LENGTH: 679
 TYPE: PRT
 ORGANISM: CANDIDATROPICALIS
 US-10-138-838-83

Query Match 10.9% Score 597; DB 9; Length 679;
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLLTPREGFVYKAKSKKI-----PLGIGIPSPTEQSAKKVKKAKENANTPLVL 485
 DB 5 KDLVYIITLIVAAVFAKNGFLDQPDGTPLINTSGSSRVLTLTKKNKNT---LL 62
 QY 486 YGSNMGTAEGBADLADIAMSK-GFAPQVATLDH---AGNLPRGAVLIYTAI-NGH 539
 DB 63 FGSQGTGAEDYANKLREHLRSRGLKTMVADFADYMDNFGDITIEDILVFFIATVGEGE 122
 QY 540 PPDNAQOVWMLQASADEKGVSVFGCGDNMTYQOKPAF---IDETLAAGAEN 596
 DB 123 PTNADPHTLWE-EDDTLSTLKYTFGLGN---STIEFFNAIGRKDRLLSEKGGDR 177
 QY 597 IADRGADASDDFEGTVEE---WREHMSDVAAYFNLD----- 631
 DB 178 FAFAE---GDDGTGLDDEDFAMKDNVFDALKNDFEELKYEPRVUKLTERDLSAA 234
 QY 632 ---IENSEDKSTLSLOFVDSADMPPLAKMHGAFSTNVVASKELQOPGASRSTRHLEL 688
 DB 235 DSQVSLGEPNKKYINSEGDILTCKG-PFDHTh-PYLARITETRELFS-SKDRHCIHVEFDI 291
 QY 669 PK-EASYOEGDHLVIRPNVEGINRVATARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746
 DB 292 SESNLKTTTGDHLAIWPSNDENIKOPAKCFGLDKLDTVLELALDSTYTPPTPTTY 351
 QY 747 EELQO-YVELQDPTVTRTOLRAMAAKTVCPRHKELEALL---EKOAYKEQVLAKRLTML 801
 DB 352 GAVIRHHLIEISGRVSRQFFLSIAG---FAPDETKKAFTRLGSGKQEPAAVTRKRNIA 408
 QY 802 ELL---EKYPACEMKFESEFIALPISIRPRYISISSPRVDEKQASITVSVSGEAMSGY 857
 DB 409 DALYSSNNAPWSVDFEFLIENVPHLTPRYISISS-SLSEKQILNVTAVVAEEADG 467
 QY 858 GEYKGIASNYLAELQ-----EGDTITCFISTP-----QSEFTLPKDPET 896
 DB 468 RPYTGVTNLLKNAVEIYONKTGEKPLVHYDLSGPRKFNKFLPVHVRNSFPLPKNSTT 527
 QY 897 PLIMVGPCTGVAAPRFGVQARQKQKQOSLGEAHLVFGCRSPHEDVLYQEE-LENAOSE 955
 DB 528 PVLIGPGTGVAPLRGFRERVOQVKNGVNKTLLFYGCGRNSNEDFLYKQEMAEVASYL 587
 QY 956 G-IITLHTAFSRMPNQPTTYQVHMEDQKLELIDOGAHFYICGDSGMAVAEATLM 1014
 DB 588 GENFEMFAPSRDPSKRVYVODKILENSQLVHLELLEGALIIYCGDASMRADVOJTIS 647
 QY 1015 KSYADVHOVSEADARLMLQOLEEKGRAVDW 1046
 DB 648 KIYAKSREISEDKAELVYKWKVQNRVQEDW 679

RESULT 14 US-10-139-031-83

Sequence 83, Application US/10139031
 Publication No. US20030049822A1
 GENERAL INFORMATION:
 APPLICANT: Wilson, Ron C.
 APPLICANT: Craft, David L.
 APPLICANT: Birch, Dudley
 APPLICANT: Eshoo, Mark
 APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.
 APPLICANT: Tang, Maria
 APPLICANT: Loper, John C.
 APPLICANT: Gleeson, Martin
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 TITLE OF INVENTION: P450 OXIDOREDUCTASE
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
 FILE REFERENCE: 1010-16
 CURRENT APPLICATION NUMBER: US/10/139,031
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US/09/976,800
 PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 83
 LENGTH: 679
 TYPE: PRT
 ORGANISM: CANDIDATROPICALIS
 US-10-138-905-83

Query Match 10.9%; Score 597; DB 9; Length 679;
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPGFVVKAKSKKI---PLGIPSPSTEOSAKVRKKAENANTPLVL 485
 DB 5 KDLVYIITLVVAAYFAKQFLDQPDPTGFLNTDGSNSRDVLLTKKNNKNT--LL 62
 QY 486 YGSMGTASTADLADIAMSK-GFAPQVATLDH---AGNLPREGAVLITVASY-NGH 539
 DB 63 FGSQGTAEADYANKLSRELHSRGLKTMVADFADYMDNFGDITIEDILVFVIATYGE 122
 QY 540 PPNNAQFVMDLQDASAEVKGVRYSVFGGDKMATTYOKVPAF---IDETLAAGAEN 596
 DB 123 PTNNADEFTWLTE-EADTSLTKTYVGLGN---STIEFFNAIGRKPRLLSEKGD 177
 QY 597 IADRGADASDDEGTVEE---WREHMSDVAAYFNLD-----631
 DB 178 FAEYAE---GDGTGLTDEDFPMAMKDNVPALKNNDLNFEEKELYPEPNVLTERRDLSA 234
 QY 632 ---IENSDNKSTLSIQFVDSADMPAKHGAFTNVVASKELQOGSARSTRHLEIEL 688
 DB 235 DSGVSLGEPKRYKINSIGDILTKG-PFDHHT-PYLARITETRELFS-SKDRHCIHVEFDI 291
 QY 689 PK-EASYOGSDHGLVPRNVEGIIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746
 DB 292 SESNLTGTDHLAIWNSDENIKOPAKCFGLDKLDVYIELKALDSTYTIPTPTTY 351
 QY 747 EELLQ-VYELQDPVTRTOLRAMAKTVCPPHKELEALL---EKQAYKEQVLAKEULTML 801
 DB 352 GAVIRHHLISGVSHPFLSIAG---FAPDEETKKAFTRLGGDKQEFPAKVRKKNFIA 408
 QY 802 ELL---EKYPACEMKSEFIALPSIRPRYYSISSPRVDEKQASITVSVSGEAMSGY 857
 DB 409 DALLYSNNAFWSADVPEFLIENVPHLTPRYYSISS-SISEKQILNVTVAEAEADG 467
 QY 858 GEYKGIASNYIAELQ-----EGDTITCFISRP-----OSEFTLPKDPET 896
 DB 468 RPYTGAVTNLKNVEIYONKTGEKPLVHYDLSGPRKFNKPLPVHRRRNFTLPKNSST 527
 QY 897 PLIMVPGTGVAPFRGFVQARKOLKEGOSLGEANHYFGCRSPHEDYLOE-LENAOSE 955
 DB 528 PVLILGPGTGVAPLRFVVERVOQVGNVGVKTLFLYGCGRNSMEDFLYKQMAEYASVL 587
 QY 956 G-IITLHTAASRPNOPKTYVOHVMEODGKLLIELDQAHFYICDGSQMAPAVEATLM 1014
 DB 588 GENFEMFNASRQDPSKRYVODKILENSQILVHELLTEGAILIYCCDASARMADVOTIS 647
 QY 1015 KSYADVHOVSEADARLMLQOLEKGRYAKDVW 1046
 DB 648 KIYAKSREISEDKAELVSKMKNRYQEDVW 679

RESULT 15
 US-10-138-905-83
 Publication 83, Application US/10138905
 GENERAL INFORMATION:
 APPLICANT: Wilson, Ron C.
 APPLICANT: Craft, David L.
 APPLICANT: Birch, Dudley
 APPLICANT: Eshoo, Mark
 APPLICANT: Madduri, Krishna M.
 APPLICANT: Cornett, Cathy A.
 APPLICANT: Brenner, Alfred A.

APPLICANT: Tang, Maria
 APPLICANT: Lopez, John C.
 APPLICANT: Gleeson, Martin
 TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
 TITLE OF INVENTION: P450 OXIDOREDUCTASE
 TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
 TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
 FILE REFERENCE: 1010-16
 CURRENT APPLICATION NUMBER: US/10/138,905
 CURRENT FILING DATE: 2002-05-03
 PRIOR APPLICATION NUMBER: US/09/976,800
 PRIOR FILING DATE: 2001-10-12
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 83
 LENGTH: 679
 TYPE: PRT
 ORGANISM: CANDIDATROPICALIS
 US-10-138-905-83

Query Match 10.9%; Score 597; DB 9; Length 679;
 Best Local Similarity 27.2%; Pred. No. 2,1e-35;
 Matches 188; Conservative 130; Mismatches 282; Indels 92; Gaps 25;

QY 430 ELDIKETLTKPGFVVKAKSKKI---PLGIPSPSTEOSAKVRKKAENANTPLVL 485
 DB 5 KDLVYIITLVVAAYFAKQFLDQPDPTGFLNTDGSNSRDVLLTKKNNKNT--LL 62
 QY 486 YGSMGTASTADLADIAMSK-GFAPQVATLDH---AGNLPREGAVLITVASY-NGH 539
 DB 63 FGSQGTAEADYANKLSRELHSRGLKTMVADFADYMDNFGDITIEDILVFVIATYGE 122
 QY 540 PPNNAQFVMDLQDASAEVKGVRYSVFGGDKMATTYOKVPAF---IDETLAAGAEN 596
 DB 123 PTNNADEFTWLTE-EADTSLTKTYVGLGN---STIEFFNAIGRKPRLLSEKGD 177
 QY 597 IADRGADASDDEGTVEE---WREHMSDVAAYFNLD-----631
 DB 178 FAEYAE---GDGTGLTDEDFPMAMKDNVPALKNNDLNFEEKELYPEPNVLTERRDLSA 234
 QY 632 ---IENSDNKSTLSIQFVDSADMPAKHGAFTNVVASKELQOGSARSTRHLEIEL 688
 DB 235 DSGVSLGEPKRYKINSIGDILTKG-PFDHHT-PYLARITETRELFS-SKDRHCIHVEFDI 291
 QY 689 PK-EASYOGSDHGLVPRNVEGIIVNRVTARFGLDASQOIRLEAE-EKLAHLPLAKTVSV 746
 DB 292 SESNLTGTDHLAIWNSDENIKOPAKCFGLDKLDVYIELKALDSTYTIPTPTTY 351
 QY 747 EELLQ-VYELQDPVTRTOLRAMAKTVCPPHKELEALL---EKQAYKEQVLAKEULTML 801
 DB 352 GAVIRHHLISGVSHPFLSIAG---FAPDEETKKAFTRLGGDKQEFPAKVRKKNFIA 408
 QY 802 ELL---EKYPACEMKSEFIALPSIRPRYYSISSPRVDEKQASITVSVSGEAMSGY 857
 DB 409 DALLYSNNAFWSADVPEFLIENVPHLTPRYYSISS-SISEKQILNVTVAEAEADG 467
 QY 858 GEYKGIASNYIAELQ-----EGDTITCFISRP-----OSEFTLPKDPET 896
 DB 468 RPYTGAVTNLKNVEIYONKTGEKPLVHYDLSGPRKFNKPLPVHRRRNFTLPKNSST 527
 QY 897 PLIMVPGTGVAPFRGFVQARKOLKEGOSLGEANHYFGCRSPHEDYLOE-LENAOSE 955
 DB 528 PVLILGPGTGVAPLRFVVERVOQVGNVGVKTLFLYGCGRNSMEDFLYKQMAEYASVL 587
 QY 956 G-IITLHTAASRPNOPKTYVOHVMEODGKLLIELDQAHFYICDGSQMAPAVEATLM 1014
 DB 588 GENFEMFNASRQDPSKRYVODKILENSQILVHELLTEGAILIYCCDASARMADVOTIS 647
 QY 1015 KSYADVHOVSEADARLMLQOLEKGRYAKDVW 1046
 DB 648 KIYAKSREISEDKAELVSKMKNRYQEDVW 679

Fri May 30 09:30:21 2003

us-10-031-241-35.rapb

Page 10

Search completed: May 29, 2003, 10:15:53
Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:01:53 ; Search time 48 Seconds
(without alignments)
2098.935 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457
Sequence: 1 TIKEMPOKTFEGELKPLPL.....RLMLQOLEEKGRYAKDVWAG 1048

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5457	100.0	1049	A34286	NADPH-ferrithemopro
2	3314	60.7	1061	D69799	cytochrome P450 /
3	3281.5	106.1	1054	A69975	NADPH-ferrithemopro
4	777.5	14.2	678	1 RDRT04	NADPH-ferrithemopro
5	769	14.1	677	1 RDPTG04	NADPH-ferrithemopro
6	769	14.1	679	2 A25505	NADPH-ferrithemopro
7	767	14.1	677	2 A60557	NADPH-ferrithemopro
8	761.5	14.0	678	2 S27158	NADPH-ferrithemopro
9	739.5	13.6	692	2 T05582	NADPH-ferrithemopro
10	737.5	13.5	681	2 T14993	NADPH-ferrithemopro
11	735.5	13.5	671	2 A56592	NADPH-ferrithemopro
12	723	13.2	601	2 A28577	NADPH-ferrithemopro
13	723	13.2	630	2 A47298	NADPH-ferrithemopro
14	711.5	13.0	683	2 T10720	NADPH-ferrithemopro
15	711	13.0	692	2 S37159	NADPH-ferrithemopro
16	709	13.0	711	2 T14081	NADPH-ferrithemopro
17	706	12.9	705	2 T10723	NADPH-ferrithemopro
18	705.5	12.9	590	2 S37157	NADPH-ferrithemopro
19	705	12.9	699	2 T14904	NADPH-ferrithemopro
20	702.5	12.9	712	2 S21531	NADPH-ferrithemopro
21	702	12.9	714	1 S31502	NADPH-ferrithemopro
22	684.5	12.5	662	2 C88451	protein K10D2.6 [1
23	683.5	12.5	1147	1 I56575	nitric-oxide synth
24	679	12.4	1429	2 JN0609	nitric-oxide synth
25	678	12.4	1429	2 S16233	nitric-oxide synth
26	677.5	12.4	1147	1 S38253	nitric-oxide synth
27	675.5	12.4	1147	1 I53165	nitric-oxide synth
28	675.5	12.4	1147	1 JCS029	nitric-oxide synth
29	675	12.4	1433	2 G01946	nitric-oxide synth

30	671.5	12.3	1147	1 S47647	nitric-oxide synth
31	669	12.3	713	2 JE0230	NADPH-cytochrome P
32	665.5	12.2	1144	1 A43271	nitric-oxide synth
33	664.5	12.2	1147	2 JCS028	nitric-oxide synth
34	661	12.1	1153	2 A49676	nitric-oxide synth
35	657.5	12.0	693	1 S38427	NADPH-ferrithemopro
36	654.5	12.0	1147	2 UC5027	nitric-oxide synth
37	654.5	12.0	1147	2 S65440	nitric-oxide synth
38	639	11.7	680	2 S63698	NADPH-ferrithemopro
39	636.5	11.7	607	2 A83726	sulfite reductase
40	628.5	11.5	605	1 G70040	sulfite reductase
41	628	11.5	680	2 S63895	NADPH-ferrithemopro
42	627.5	11.5	506	2 S37156	NADPH-ferrithemopro
43	617.5	11.3	710	2 JC7192	NADPH-ferrithemopro
44	614.5	11.3	1247	2 T31331	nitric-oxide synth
45	608.5	11.2	1203	1 A47501	nitric-oxide synth

ALIGNMENTS

RESULT 1

A34286 NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - Bacillus megaterium
N/Contains: NADPH-ferrithemoprotein reductase (EC 1.6.2.4); unspecific monooxygenase (EC
C/Species: Bacillus megaterium
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
C/Accession: A34286; S43653
R/Ruettiger, R.T.; Wen, L.P.; Fulco, A.J.
J. Biol. Chem. 264, 10987-10995, 1989
A/Title: Coding nucleotide, 5' regulatory, and deduced amino acid sequences of P-450-BM-
A/Reference number: A34286; MUID:89291834; PMID:2544578
A/Accession: A34286
A/Molecule type: DNA
A/Residues: 1-1049 <RUE>
A/Cross-references: GB:04832; MID:g142797; PID:AAA87602.1; PID:g142798
R/Munro, A.W.; Lindsey, J.G.; Cogging, J.R.; Kelly, S.M.; Price, N.C.
FEBS Lett. 343, 70-74, 1994
A/Title: Structural and enzymological analysis of the interaction of isolated domains of
A/Reference number: S43653; MUID:94215710; PMID:8163021
A/Accession: S43653
A/Molecule type: Protein
A/Residues: 430-439; 441-496 <MCN>
C/Genetics:
A/Gene: CYP102
C/Superfamily: P450 bifunctional enzyme CYP102; Cytochrome P450 homology; flavodoxin hom
C/Keywords: chromoprotein; electron transfer; FAD; flavoprotein; FMN; heme; iron; metallo
F/262-423/Domain: cytochrome P450 homology <P45>
F/483-1046/Domain: NADPH-ferrithemoprotein reductase homology <FEH>
F/485-622/Domain: flavodoxin homology <FLX>
F/401/Binding site: heme iron (Cys) (axial ligand) #status predicted.

Query Match 100.0%; Score 5457; DB 1; Length 1049;
Best Local Similarity 100.0%; Pred. No. 3.1e-298;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TIKEMPOKTFEGELKPLPLNTDQVQALMKIDELGEIKFPAQGVTVRYLSQRILKE	60
DB	2	TIKEMPOKTFEGELKPLPLNTDQVQALMKIDELGEIKFPAQGVTVRYLSQRILKE	61
QY	61	ACDESREDFKSLQALKFVRDPADGGLFTSWTHKMKKANHLLPSFSQAMKGYHAMV	120
DB	62	ACDESREDFKSLQALKFVRDPADGGLFTSWTHKMKKANHLLPSFSQAMKGYHAMV	121
QY	121	DIIVQVQKWERLUNADDEHIVPEDMRLTLDTIGLGCFFNRFNSFYRDQHPFTTSWRA	180
DB	122	DIIVQVQKWERLUNADDEHIVPEDMRLTLDTIGLGCFFNRFNSFYRDQHPFTTSWRA	181
QY	181	LIDAMNKLQKANDDDPAYDENKRFQEDIKVMDLVDKIIADRKASGEQSDLLTHMLNG	240
DB	182	LIDAMNKLQKANDDDPAYDENKRFQEDIKVMDLVDKIIADRKASGEQSDLLTHMLNG	241
QY	241	KDETEGPELDENIRYQIITFLIAGHETTSGLSFALYFLVKNPHYLQKAAEAARVLVD	300

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|||||
242 KDPETGSPLDENIRYQITFLTLAGHETTSGLTSPALFLVKNHVLQKAEEARVLVD 301
QY PVPEYKVKOLKQVGMVNEALRLMPPTAPSLVAKETVYGGVPLEKGEMLVLLPOL 360
Db PVPEYKVKOLKQVGMVNEALRLMPPTAPSLVAKETVYGGVPLEKGEMLVLLPOL 361
QY HRDRTIMGDDVEEERPERFENPSAIPQHAFFPGNGORACIGQOFALHEATLVLMMLKH 420
Db HRDRTIMGDDVEEERPERFENPSAIPQHAFFPGNGORACIGQOFALHEATLVLMMLKH 421
QY 421 FDFEDHTNYELDIKETTLTKPEGFVVKAKSKKIPLGIPSPSTQSAKVKKAKENAMNT 480
Db 422 FDFEDHTNYELDIKETTLTKPEGFVVKAKSKKIPLGIPSPSTQSAKVKKAKENAMNT 481
QY 481 PLVLVGSNMGCTAGTARDLADLAMSKEGAPQVATLDSHAANLPRGAVLVTASYNHR 540
Db 482 PLVLVGSNMGCTAGTARDLADLAMSKEGAPQVATLDSHAANLPRGAVLVTASYNHR 541
QY 541 PDNAKQFVMDLQASADEVKGVRSVFGCGDKNMATTYQKPAFIDETLAKGAENIADR 600
Db 542 PDNAKQFVMDLQASADEVKGVRSVFGCGDKNMATTYQKPAFIDETLAKGAENIADR 601
QY 601 GEADASDDEFGTYEERHWMMSDVAAVFNLDIENSNDKSTLSIQFVDSAADMLAKMHG 660
Db 602 GEADASDDEFGTYEERHWMMSDVAAVFNLDIENSNDKSTLSIQFVDSAADMLAKMHG 661
QY 661 AFSNNVASKELQOPGASRSTRHLEIELPKASVOEGDHLGVIPRNYGIVNRTARFGL 720
Db 662 AFSNNVASKELQOPGASRSTRHLEIELPKASVOEGDHLGVIPRNYGIVNRTARFGL 721
QY 721 DASQOIRLEAEBEKLAHLPLAKTVSVEELLQVVELQVDPVTRTOLRAMAKTVCPHKKEL 780
Db 722 DASQOIRLEAEBEKLAHLPLAKTVSVEELLQVVELQVDPVTRTOLRAMAKTVCPHKKEL 781
QY 781 EALLEKQAYKEQVLAKRITMLLELEKYPACEMKSEFALLIPSRPRYSSISSPRVDEK 840
Db 782 EALLEKQAYKEQVLAKRITMLLELEKYPACEMKSEFALLIPSRPRYSSISSPRVDEK 841
QY 841 QASTTVSVSGEAMSGVEYGVGSIASNYLAELQEGTTCFSTPQSEETLRKDPETPLIM 900
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QY 901 VGPETGVAPFRFGVQARQOLKEQOGLGEALHYFCRSPHEDYLYQOELENASQEGITTL 960
Db 902 VGPETGVAPFRFGVQARQOLKEQOGLGEALHYFCRSPHEDYLYQOELENASQEGITTL 961
QY 961 HTAFSRMPNQRTTYQVHVEDGKKLIELLDQGAHFYICGDSGOMAPAVEATLMKSYADV 1020
Db 962 HTAFSRMPNQRTTYQVHVEDGKKLIELLDQGAHFYICGDSGOMAPAVEATLMKSYADV 1021
QY 1021 HOVSEADARLWLQOLEEKGRYAKDVWAG 1048
Db 1022 HOVSEADARLWLQOLEEKGRYAKDVWAG 1049

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RESULT 2

D69799

cytochrome P450 / NADPH-cytochrome P450 r homolog yeto - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000

C/Accession: D69799

R/Kunst, F.; Ogasaawa, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funo, S.; Galizzi, A.; Galler

leach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, W.; Sato, T.; Scanlon, T.; Scanton,

A/Authors: Schleich, S.; Schroeter, R.; Scifione, R.; Sekiguchi, J.; Sekowska, A.; Serot

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akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zunshtet, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: D69799
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Restrictions: 1-1061 <RUN>
A/Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12544.1; PID:g2633038
A/Experimental source: strain 168
A/Genetics:
A/Gene: yeto
C/Superfamily: P450 bifunctional enzyme CYP102; cytochrome P450 homology; flavodoxin hom
C/Keywords: chromoprotein; flavoprotein; heme; iron; metalloprotein
F:264-425/Domain: cytochrome P450 homology <P45>
F:493-1057/Domain: NADPH-ferrithemoprotein reductase homology <FEH>
F:495-632/Domain: Flavodoxin homology <FLX>
F:403/Binding site: heme iron (Cys) (axial ligand) #status predicted

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Query Match 60.7%; Score 3314; DB 2; Length 1061;

Best local similarity 59.5%; Pred. No. 5, 7e-178; Matches 628; Conservative 156; Mismatches 259; Indels 12; Gaps 6;

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QY 5 MPQKTFGEELKUNPLINTDKRVOALMKIADDELGEFKEAPGRVTRYLSQRLIKEACDE 64
Db 7 IPQKTFGPIGNPLIKDKPRTSLIKLAEQGPFIQHTPAGTIVVSGHELVKEVDE 66
QY 65 SRPKNLSQALKPRDAGGGLFTSWTHKQWKAHNLILPSPQOMKGYHAMVULIAY 124
Db 67 ERFPKSLIEGALKERASGGGLFTSWTHKQWKAHNLILPSPQOMKGYHAMVULIAY 126
QY 125 QLVQKMERLANDEHIEVPEDMTLRLTDITGICGFNFNSFSDQPHFTSMWRALDEA 184
Db 127 QLVQKMERLANDEHIEVPEDMTLRLTDITGICGFNFNSFSDQPHFTSMWRALDEA 186
QY 185 MNKLQANPDDPAYDENKROFQEDIKVMDLVKIIADKASGEQSD-DLTHMLNKDP 243
Db 187 MNKLQANPDDPAYDENKROFQEDIKVMDLVKIIADKASGEQSD-DLTHMLNKDP 246
QY 244 ETGEPPLDDENIRYQITFLTLAGHETTSGLTSPALFLVKNHVLQKAEEARVLVDVP 303
Db 247 ETGEPPLDDENIRYQITFLTLAGHETTSGLTSPALFLVKNHVLQKAEEARVLVDVP 306
QY 304 SYKQKOLKQVGMVNEALRLMPPTAPSLVAKETVYGGVPLEKGEMLVLLPOLARD 363
Db 307 SYKQKOLKQVGMVNEALRLMPPTAPSLVAKETVYGGVPLEKGEMLVLLPOLARD 366
QY 364 KTIWGDVEEERPERFENPSAIPQHAFFPGNGORACIGQOFALHEATLVLMMLKHDF 423
Db 367 KTIWGDVEEERPERFENPSAIPQHAFFPGNGORACIGQOFALHEATLVLMMLKHDF 426
QY 424 EDHTNYELDIKETTLTKPEGFVVKAKSKKIPLGIPSPSTQSAKVKKAKENAMNT 477
Db 427 EDHTNYELDIKETTLTKPEGFVVKAKSKKIPLGIPSPSTQSAKVKKAKENAMNT 480
QY 478 --HNTPLVLVYGSNMGCTAGTARDLADLAMSKEGAPQVATLDSHAANLPRGAVLVTAS 535
Db 487 GIANRPLVLVYGSNMGCTAGTARDLADLAMSKEGAPQVATLDSHAANLPRGAVLVTAS 546
QY 536 YNGHPDNNAKQFVMDLQASADEVKGVRSVFGCGDKNMATTYQKPAFIDETLAKGA 595
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QY 596 NIARGEADSDDEFGTYEERHWMMSDVAAVFNLDI-ENSEDNKSTLSIQFVDSAADMP 654
Db 607 NIARGEADSDDEFGTYEERHWMMSDVAAVFNLDI-ENSEDNKSTLSIQFVDSAADMP 666
QY 655 LAKHGAFTTVVASKELQOPGASRSTRHLEIELPKASVOEGDHLGVIPRNYGIVNRT 714
Db 667 LAKHGAFTTVVASKELQOPGASRSTRHLEIELPKASVOEGDHLGVIPRNYGIVNRT 726
QY 715 TARPGLDASQOIRLEAEBEKLAHLPLAKTVSVEELLQV-VELQVDPVTRTOLRAMAKTV 773

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biochemistry 29, 9814-9818, 1990

A:Title: NADPH-cytochrome P-450 oxidoreductase gene organization correlates with structure

A:Reference number: A36073; MUID:91104888; PMID:2125483

A:Accession: A36073

A:Molecule type: DNA

A:Residues: 1-678 <PO2>

A:Cross-references: GB:J05291

R:Porter, T.D.; Kasper, C.B.

Proc. Natl. Acad. Sci. U.S.A. 82, 973-977, 1985

A:Title: Coding nucleotide sequence of rat NADPH-cytochrome P-450 oxidoreductase cDNA and

A:Reference number: A00402; MUID:85140278; PMID:3919392

A:Accession: A00402

A:Molecule type: mRNA

A:Residues: 1-678 <POR>

A:Cross-references: GB:M10068; NID:g203872; PIDN:AAAA1064.1; PID:g203873

R:Mutakami, H.; Yabuuchi, Y.; Ohkawa, H.

DNA 5, 1-10, 1986

A:Title: Expression of rat NADPH-cytochrome P-450 reductase cDNA in Saccharomyces cerevisiae

A:Reference number: A25813; MUID:86163762; PMID:3082610

A:Accession: A25813

A:Molecule type: mRNA

A:Residues: 1-678 <MOR>

A:Cross-references: GB:M12516; NID:g203878; PIDN:AAA41067.1; PID:g203879

C:Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of FMN and to bacterial flavodoxins.

C:Genetics:

A:Introns: 60/2; 76/3; 119/3; 169/3; 211/2; 241/2; 274/2; 313/2; 353/1; 413/3; 463/3; 553/3; 583/3; 603/3; 623/3; 643/3; 663/3; 683/3; 703/3; 723/3; 743/3; 763/3; 783/3; 803/3; 823/3; 843/3; 863/3; 883/3; 903/3; 923/3; 943/3; 963/3; 983/3; 1003/3; 1023/3; 1043/3; 1063/3; 1083/3; 1103/3; 1123/3; 1143/3; 1163/3; 1183/3; 1203/3; 1223/3; 1243/3; 1263/3; 1283/3; 1303/3; 1323/3; 1343/3; 1363/3; 1383/3; 1403/3; 1423/3; 1443/3; 1463/3; 1483/3; 1503/3; 1523/3; 1543/3; 1563/3; 1583/3; 1603/3; 1623/3; 1643/3; 1663/3; 1683/3; 1703/3; 1723/3; 1743/3; 1763/3; 1783/3; 1803/3; 1823/3; 1843/3; 1863/3; 1883/3; 1903/3; 1923/3; 1943/3; 1963/3; 1983/3; 2003/3; 2023/3; 2043/3; 2063/3; 2083/3; 2103/3; 2123/3; 2143/3; 2163/3; 2183/3; 2203/3; 2223/3; 2243/3; 2263/3; 2283/3; 2303/3; 2323/3; 2343/3; 2363/3; 2383/3; 2403/3; 2423/3; 2443/3; 2463/3; 2483/3; 2503/3; 2523/3; 2543/3; 2563/3; 2583/3; 2603/3; 2623/3; 2643/3; 2663/3; 2683/3; 2703/3; 2723/3; 2743/3; 2763/3; 2783/3; 2803/3; 2823/3; 2843/3; 2863/3; 2883/3; 2903/3; 2923/3; 2943/3; 2963/3; 2983/3; 3003/3; 3023/3; 3043/3; 3063/3; 3083/3; 3103/3; 3123/3; 3143/3; 3163/3; 3183/3; 3203/3; 3223/3; 3243/3; 3263/3; 3283/3; 3303/3; 3323/3; 3343/3; 3363/3; 3383/3; 3403/3; 3423/3; 3443/3; 3463/3; 3483/3; 3503/3; 3523/3; 3543/3; 3563/3; 3583/3; 3603/3; 3623/3; 3643/3; 3663/3; 3683/3; 3703/3; 3723/3; 3743/3; 3763/3; 3783/3; 3803/3; 3823/3; 3843/3; 3863/3; 3883/3; 3903/3; 3923/3; 3943/3; 3963/3; 3983/3; 4003/3; 4023/3; 4043/3; 4063/3; 4083/3; 4103/3; 4123/3; 4143/3; 4163/3; 4183/3; 4203/3; 4223/3; 4243/3; 4263/3; 4283/3; 4303/3; 4323/3; 4343/3; 4363/3; 4383/3; 4403/3; 4423/3; 4443/3; 4463/3; 4483/3; 4503/3; 4523/3; 4543/3; 4563/3; 4583/3; 4603/3; 4623/3; 4643/3; 4663/3; 4683/3; 4703/3; 4723/3; 4743/3; 4763/3; 4783/3; 4803/3; 4823/3; 4843/3; 4863/3; 4883/3; 4903/3; 4923/3; 4943/3; 4963/3; 4983/3; 5003/3; 5023/3; 5043/3; 5063/3; 5083/3; 5103/3; 5123/3; 5143/3; 5163/3; 5183/3; 5203/3; 5223/3; 5243/3; 5263/3; 5283/3; 5303/3; 5323/3; 5343/3; 5363/3; 5383/3; 5403/3; 5423/3; 5443/3; 5463/3; 5483/3; 5503/3; 5523/3; 5543/3; 5563/3; 5583/3; 5603/3; 5623/3; 5643/3; 5663/3; 5683/3; 5703/3; 5723/3; 5743/3; 5763/3; 5783/3; 5803/3; 5823/3; 5843/3; 5863/3; 5883/3; 5903/3; 5923/3; 5943/3; 5963/3; 5983/3; 6003/3; 6023/3; 6043/3; 6063/3; 6083/3; 6103/3; 6123/3; 6143/3; 6163/3; 6183/3; 6203/3; 6223/3; 6243/3; 6263/3; 6283/3; 6303/3; 6323/3; 6343/3; 6363/3; 6383/3; 6403/3; 6423/3; 6443/3; 6463/3; 6483/3; 6503/3; 6523/3; 6543/3; 6563/3; 6583/3; 6603/3; 6623/3; 6643/3; 6663/3; 6683/3; 6703/3; 6723/3; 6743/3; 6763/3; 6783/3; 6803/3; 6823/3; 6843/3; 6863/3; 6883/3; 6903/3; 6923/3; 6943/3; 6963/3; 6983/3; 7003/3; 7023/3; 7043/3; 7063/3; 7083/3; 7103/3; 7123/3; 7143/3; 7163/3; 7183/3; 7203/3; 7223/3; 7243/3; 7263/3; 7283/3; 7303/3; 7323/3; 7343/3; 7363/3; 7383/3; 7403/3; 7423/3; 7443/3; 7463/3; 7483/3; 7503/3; 7523/3; 7543/3; 7563/3; 7583/3; 7603/3; 7623/3; 7643/3; 7663/3; 7683/3; 7703/3; 7723/3; 7743/3; 7763/3; 7783/3; 7803/3; 7823/3; 7843/3; 7863/3; 7883/3; 7903/3; 7923/3; 7943/3; 7963/3; 7983/3; 8003/3; 8023/3; 8043/3; 8063/3; 8083/3; 8103/3; 8123/3; 8143/3; 8163/3; 8183/3; 8203/3; 8223/3; 8243/3; 8263/3; 8283/3; 8303/3; 8323/3; 8343/3; 8363/3; 8383/3; 8403/3; 8423/3; 8443/3; 8463/3; 8483/3; 8503/3; 8523/3; 8543/3; 8563/3; 8583/3; 8603/3; 8623/3; 8643/3; 8663/3; 8683/3; 8703/3; 8723/3; 8743/3; 8763/3; 8783/3; 8803/3; 8823/3; 8843/3; 8863/3; 8883/3; 8903/3; 8923/3; 8943/3; 8963/3; 8983/3; 9003/3; 9023/3; 9043/3; 9063/3; 9083/3;

Oy		877	-ITCFSTPOSEETLTKDPETPLIMYGPNGVAPFRGFVARAKOLKQGGISGAHLY	933
Dd		506	RALVPMPFR--KSQRLLPFKSTTPYMVGPGIGIARPFMGFIGERALLRRQGKVGETILLY	563
Oy		934	FGRSPHEHYLYOELENAOSEGIT-LHTAFSRMNPQXTYVOHVMEODGKLIELLDQ	992
Dd		564	YGCRRSDDDYLYREELRAFHHDKAGALTQLNVASFR-EQAHKVVYOHLKKREDRLHWLKIHIE	622
Oy		993	-GARFYVCQDGSQMAPVAEATLMKSYADVHQVSSEADARLMLDLQEEKGYAKXWMA	1047
Dd		623	GGAHIYYCGDRRNNAKDVTONTFYDIVAEFGPEFHQTAVDVVKLTMTKGRISLDWMS	678
<p style="text-align:center;">RESULT 5 RDPG04</p>				
NADPH-ferrithemoprotein reductase (EC 1.6.2.4) - pig				
NAlternate names: NADP-cytochrome P450 reductase				
CSpecies: Sus scrofa domestica (domestic pig)				
CDate: 04-Dec-1986 #sequence_revision 03-Feb-1994 #ext_change 03-Jun-2002				
CAccession: A25584; A00403				
C/Hanlu, M.; Iyanagi, T.; Miller, P.; Lee, T.D.; Shively, J.E.				
Biochemistry 25, 7906-7911, 1986				
A>Title: Complete amino acid sequence of NADPH-cytochrome P-450 reductase from porcine he				
AReference number: A25584; MID:87101085; EMD:3099837				
AAccession: A25584				
AMolecule type: protein				
AResidues: 1-677 <HAN>				
R/Vogel, F., Lumber, L.				
Biochem. J. 236, 871-878, 1986				
A>Title: Complete structure of the hydrophilic domain in the porcine NADPH-cytochrome P-				
AReference number: A00403; MID:87073664; EMD:3098240				
ACcession: A00403				
AMolecule type: protein				
AResidues: 56-162, 'S', 164-173, 'D', 175-338, 'A', 340-377, 'D', 379-399, 'E', 401-445, 'L', 447-50				
CSuperfamily: NADPH-ferrithemoprotein reductase; Flavodoxin homology; NADPH-ferrithemopro				
CKeywords: acetylated amino end; electron transfer; endoplasmic reticulum; PAD; flavopte				
F76-126/Domain: FMN binding <FMN>				
F79-675/Domain: NADPH-ferrithemoprotein reductase homology <FEH>				
F/81-223/Domain: flavodoxin homology <FLX>				
F/451-476/Domain: PAD binding <PAD>				
F/Modified site: acetylated amino end (Gly) #status experimental				
<p style="text-align:center;">Query Match 14.1%; Score 769; DB 1; Length 677; Best Local Similarity 31.9%; Pred.No.1.9e-35; Matches 224; Conservative 109; Mismatches 275; Indels 94; Gaps 27;</p>				
Oy		401	IGOOFPALHEAT-----LVLGMMLRHPDEEDTNY--ELDILETLT-LKPESGVVAKS	450
Dd		15	VABEVSLTSATDMVLFSLIIVGLTYWFIRPKKKDEVPEPSKIETTSSVXDSSF-----	69
Oy		451	KPIPLGIIPSTEOSAKVRKKAENAHNTPLLVLVYSNMGTREGTARDLADIAMSQFA	510
Dd		70	-----EKMKKTGRN-----IIVFSGSQTAEEPRANLSKDAHRGMR	107
Oy		511	POVALTD---SHAGNLPR-EGAVLI-VTASY-NGHPPNNAKOFVWLDOASDEVKGV	563
Dd		108	GMAADPEERYDSLSSLBEIENALAVFCMATYTGEQPTDNADOFTMYMLEADVD-LTGVK	166
Oy		564	YSVFCGDKNMATTYQKYPA---FIDETLAAGAENIAADRGADASDFEGTYEWNRHM	620
Dd		167	YAIFGLGNK---TEHFENAMGVYDKRLBOUGAQRIFDLGDDDGNDLEEDFITWREOF	222
Oy		621	MSDVAAYTNLDENSEDKSTLSLOF---VDSAA-----DMPLAKMHGAFS	663
Dd		223	WPACEHGVEVTEGESSTRQVELVHTDMTRAVVTTGEMGRKLSYENOKEPPDAKNPFL	282
Oy		664	TNVASKELQOPGARSRTHEIEL-PKEASTOEGDHLCVIPPNYIGIVARTARFGLDA	722
Dd		283	AVVTTNRKLNO-GTERHLMHELDLSDSKIRRESGSHVAVYPANDSALVNQDELIGTDL	341
Oy		723	SQQI---RLAEERKLAHLPLAKTVSVBELLOYVELQDVTQTQLRAMAAKTCPPHKVE	779
Dd		342	DIVSNLNIDESENKRHPGPCPTYRT-ALTYYLDITNRPRTNVLEVLMQVASEPSEOQ	400

QY 780 LEALLB-----KOAYKEOVLAKRLTLMLELEKYPACEMKFESEFIALPISIRPRYSISS 834
 Db 401 LRMASSSGGKELYSWVVEARRHILAILQDYPRLRPIDHLCERLPRLOARYSIASS 460
 QY 835 PRVDEKQASITTVSVSGEAMSGYGEYKGIASNYL-AELOQDGT-----ITCFISTPOSEF 888
 Db 461 SKHAPNSVHICAAVVEYETKSGRYN-KGVATSWLRAPKAPENGRRALVPMFVR--KSOQ 517
 QY 889 TLKDEPPLIMVPGGVAPPRFGVQARKOLKEOGSGLEAMHIFGCRSPHEDYLXOE 948
 Db 518 RLFPFKATTPVIMVPGGVAPPRFGVQARKOLKEOGSGLEAMHIFGCRSPHEDYLXOE 577
 QY 949 LENAQSEGIT-LHTAFSRMPNOP-KTYVQVHMEODGSKLIELL-DOGAFFYICGDSQOM 1005
 Db 578 LAQFPAKALTRLSVANR--EQQKAYVQHLKRDKEHMKLHDSGAHIIYICGDARNM 635
 QY 1006 APVAVETLMKSYADVHOVSEADARLWLOOLEEKRYAKDYWA 1047
 Db 636 ARDVONTFCDIVABOQFMEHAQADVYKCLMTKGRVSLDWMS 677

RESULT 6

A25505
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 03-Jun-2002
 C/Accession: A25505; A05233
 R/Katagiri, M.; Murakami, H.; Yabusaaki, Y.; Sugiyama, T.; Okamoto, M.; Yamano, T.; Ohkaw
 J.; Biochem. 100, 945-954, 1986
 A/Title: Molecular cloning and sequence analysis of full-length cDNA for rabbit liver NA
 A/Reference number: A25505; MUID:87137361; PMID:3029050
 A/Accession: A25505
 A/Molecule type: mRNA
 A/Residues: 1-679 <KAT>
 A/Cross-references: GB:X04610; NID:91543; PIDN:CA28279.1; PID:91544
 R/Black, S.D.; Coon, M.J.
 J. Biol. Chem. 257, 5929-5938, 1982
 A/Title: Structural features of liver microsomal NADPH-cytochrome P-450 reductase. Hydric
 A/Reference number: A05233; MUID:82167456; PMID:6802823
 A/Accession: A05233
 A/Molecule type: protein
 A/Residues: PTHGG, 14-39, 'NY', 42-52, 'N', 54-81 <BLA>
 A/Note: the order of the first four residues was not determined
 C/Note: the amino end of the mature protein is acetylated
 C/Comment: This enzyme, a membrane-bound flavoprotein containing one molecule each of FM
 C/Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprot
 C/Keywords: acetylated amino end; electron transfer; FAD; flavoprotein; FMN; membrane pr
 F/1-56/Domain: membrane-bound #status predicted <MEM>
 F/78-228/Domain: FMN binding #status predicted <FMN>
 F/81-677/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F/83-225/Domain: flavodoxin homology <FLX>
 F/85-96/Region: FMN-phosphate binding #status predicted
 F/288-327,453-478/Domain: FAD binding #status predicted <FAD>
 F/294-297/Region: FAD-pyrophosphate binding #status predicted

Query Match 14.1%; Score 769; DB 2; Length 679;
 Best Local Similarity 31.7%; Pred. No. 1.9e-35;

Matches 212; Conservative 111; Mismatches 250; Indels 96; Gaps 24;

QY 444 FVYAKSKKIP-----LQGISPSTQGA--KVRKKKNAHNPPLVLYGSMNGTAEGTA 497
 Db 42 FLPRKKKEVEBFTKIQAPRTSSVKESSFVEKKKTKRNN-----IVFYGSGGTAEFA 96
 QY 498 RLADLADIMSGFAPQVATLDSH---AGNIPREGAVITV--TASY-NGHPPDNKKQFVW 550
 Db 97 NRTLSKHAHRYGMGMADPREYDLADLSLPEINNALAVCMATYVGGEDPTDNOAFYDW 156
 QY 551 LDOASADEVGVRSYVFCGDKXWATTYQKVP---FIDEFLAKGAKENIADGEADASD 607
 Db 157 LQETDND-LSGVTKAYVGLGNK-----TYEFNPMGKTVQDRLEGLGQRIFEIGMGDDDA 211
 QY 608 DFEQTYEWEHMHMSDVAAAYFNLDIENSEDNKSTLSIQFVDSADAMELATQH----- 659

Db 212 NLEDEFTWREQFWPAVCEHFGEATGEESISIQVEYLVL---HTDIDVAKVYOGEMGRLK 268
 QY 660 -----GAFSTNVASKELELOQPGSARSTRLEIEL-PKENSYOGCHILGYIPRN 706
 Db 269 SYENQKPPEDAKNPFLATYTNKRLNO-GTERLHMLELDI SDSKIRYESGDHVAAYPAN 327
 QY 707 YEGIVARVTARFGLDASQOI---RLBAEEKLALHPL-----AKTVSV 746
 Db 328 DSAVLVQGLGILLGADLDVWMSLNNDLESKHKHPFCPSYRTALTYIDITNPRNTVL 387
 QY 747 BEILOQVELQDPTVKTQLRAMAATVCPPHKVELLEALKOAYKEOVLAKRLTLMLELEK 806
 Db 388 YELAQVA--ADPAEQQLRKMMASSG-----EGKELYLSWVVEARRHILAILQD 434
 QY 807 YPACEMKFESEFIALPISIRPRYSISSPRVDEKQASITTVSVSGEAMSGYGEYKGIASN 866
 Db 435 YPSLRPPIDHLCERLPRLOARYSIASSKVPNSVHICAAVVEYETKAGRLN-KGVATS 493
 QY 867 YL-AELOQDGT-----ITCFISTPOSEFTLPKDEPPLIMVPGGVAPPRFGVQARKOL 920
 Db 494 WLRAPKAPENGRRALVPMFVR--KQFRLPFAATTPVIMVPGGVAPPRFGVQARKOL 551
 QY 921 KEQGSGLGEAHLYFGCRSPHEDYLXOELENAQSEGIT-LHTAFSRMPNOPRTYVQVHM 979
 Db 552 ROQKEVGETLTYGCGRAAEDLYLREBELAGFQKDGTLSQLNVAFSRQAO-KVYVQHL 610
 QY 980 EDOGKLIETLDD-GAHFYICGSGSOMAPVAVETLMKSYADVHOVSEADARLWLOOLEEK 1038
 Db 611 RRKEHLMRLIHGGAHYVCGDARNWARDVONTFYDIVAELGAMHAQADVYKCLMTK 670
 QY 1039 GRVAKDYWA 1047
 Db 671 GRVSLDWMS 679

RESULT 7

A60557
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - human
 N/Alternate names: NADP-cytochrome P450 reductase
 C/Species: Homo sapiens (man)
 C/Date: 17-Apr-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002
 C/Accession: A33421; A60557; S21686
 R/Haniu, M.; McManus, M.E.; Birkett, D.J.; Lee, T.D.; Shively, J.E.
 Biochemistry 28, 8639-8645, 1989
 A/Title: Structural and functional analysis of NADPH-cytochrome P-450 reductase from hu
 A/Reference number: A33421; MUID:90105350; PMID:2513880
 A/Accession: A33421
 A/Molecule type: protein
 A/Residues: 2-677 <HAN>
 A/Note: 551-Gln was also found
 R/Yamano, S.; Aoyama, T.; McBride, O.W.; Hardwick, J.P.; Gelboin, H.V.; Gonzalez, F.J.
 Mol. Pharmacol. 36, 83-88, 1989
 A/Title: Human NADPH-P450 oxidoreductase: complementary DNA cloning, sequence and vaccin
 A/Reference number: A60557; MUID:89313720; PMID:2501655
 A/Accession: A60557
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-137, 'G', 139-577, 'DV', 580-677 <YAN>
 R/Shepherd, E.A.; Palmer, C.N.A.; Segall, H.J.; Phillips, I.R.
 Arch. Biochem. Biophys. 294, 168-172, 1992
 A/Title: Quantification of cytochrome P450 reductase gene expression in human tissues.
 A/Reference number: S21686; MUID:92198003; PMID:1550342
 A/Accession: S21686
 A/Molecule type: mRNA
 A/Residues: 2-499, 'V', 501-517, 'L', 519-536, 'WH', 539-677 <SHE>
 A/Cross-references: GB:S90469; NID:9247306; PIDN:AA321814.1; PID:9247307
 C/Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprot
 C/Keywords: acetylated amino end; electron transfer; endoplasmic reticulum; FAD; flavoprc
 F/1-56/Domain: membrane-bound #status predicted <MEM>
 F/2-677/Product: NADPH-ferrihemoprotein reductase #status experimental <MAT>
 F/77-227/Domain: FMN binding #status predicted <FMN>
 F/80-675/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:82-224/Domain: flavodoxin homology <FLX>
 F:84-95/Region: FMN-phosphate binding #status predicted <FAD>
 F:267-326,452-477/Domain: FAD binding #status predicted <FAD>
 F:293-296/Region: FAD-pyrophosphate binding #status predicted
 F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
 F:566/Binding site: NADP (Cys) #status experimental

Query Match 14.1%; Score 767; DB 2; Length 677;
 Best Local Similarity 32.4%; Pred. No. 2.5e-35;
 Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;

QY 444 FVYAKSKKIP-----LGIPTSPSTEQS-AKVYKKAENANHTPLVLVYSGNMGTAEGR 498
 DB 42 FLFRKKKEEPEFTKISTTTSSVKESSFVKKMKKTGRN-----IIFYGSGTGAEEFAN 96
 QY 499 DLADIAMSKGAPAVATLDH-----AGNLPRGAVLTASY-NGHPPDNKQFVDWL 551
 DB 97 RLSDKHRYGMRGMAADPEEYDLADLSLPEIDNLAFCMATYGEEDPTNADQFYDWL 156
 QY 552 DQASDEVKGVYVFGCGDKMATTYQKVP---FIDETLAAGAENIADRGADASDD 608
 DB 157 QETDVL-DLSGVKAVFGLGNK---TYEHFAMKQYVDKLEQAGQRIFFELGDDGDN 211
 QY 609 FEGTYEEMHMSDVAAVFNLDIENSDNKSTLSLOF---VDSA---ADMLAKMH- 659
 DB 212 LEBDFITWREQFWPVCHEFVEATGEESIRQYELVHTDIDAKVYMGEMGRKSYEN 271
 QY 660 -----GAFSTNVVASKELQPGASRSTRHLEIEL-PKEASYOEGDHLVIRNYEGI 710
 DB 272 QKPPFDANKPFLAATVTRKLNQ-GTERHLMHLELDSDSKIRYESGDHVAVVPANDSNL 330
 QY 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEVELLYQVELODPVTRTOLRAMA 768
 DB 331 VNQGLKLGADLVVMSLNINDESNKNGPRPCPTSYRTALTYLDITNP-PRTNVLYEL 389
 QY 769 AKTYCPRHKEVLEALLE-----KQAYKEQVLAKRLTMLELLEKYPACENKFSFIALLP 822
 DB 390 AQVASESEBQELHKKMASSGEGKELYLWVVEARRHIALILOCPSLRPIIDHLCILLP 449
 QY 823 SIRRYYSISSPPVDEKQASITVSVSGEAMSGYGEYKGIASNYL-AELOEGDT----- 876
 DB 450 RLQARYSIASSKVNHSVHICAVVVEYETKGRIN-KGVAITWMLKPEAPAGEGRAL 508
 QY 877 ITCTISTPOSEFTLPKDPETPLIMVPGTGVAPFRGVQARKOLKEGOSLGEAHLFYGC 936
 DB 509 VPMFVR--KSQFRLPEFKATTPVIMVGPSTGVAFFIGTQERAWLQQGKEVGETLLYYGC 566
 QY 937 RSPHEDLYOELENAQSEGIIT-LHTAFSRMPNQPTVYQVHMEODGKLIIELDQGAH 995
 DB 567 RRSDELYREBELAQFHRDGLTQLNVAFSREOSH-KVYVOHLLKODREHLMKLEGGAH 625
 QY 996 FYICGDSQMAPAVEATLTKMSYADVHOVSEADARLMLQOLEKGRYAKDVMA 1047
 DB 626 IYVCGDARNMARDVONTFYDVAELGMEHQAADVYKKLMTKGRISLDVMS 677

RESULT 8

S27158
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) - guinea pig
 N:Alternate names: NADPH-cytochrome P450 oxidoreductase
 C:Species: *Cavia porcellus* (guinea pig)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
 C:Accession: S27158; #38510
 R:Obtainer: S. J. Goda, T. J. Ishizaki, K. J. Kametaki, T. J. Shintake, N. J. Shintake
 A:Title: Molecular cloning and sequence analysis of mouse NADPH-cytochrome P-450 oxidoreductase
 A:Reference number: S27158; MUID:93041995; PMID:1420354
 A:Accession: S27158
 A:Molecule type: mRNA
 A:Residues: 1-678 <OHG>
 A:Cross-references: EMBL: D10498; NID: g220556; PIDN: BAA01385.1; PID: g220557
 A:Note: the species identification has been revised in reference S38510
 R:Obtainer: S. J. Goda, T. J. Ishizaki, K. J. Kametaki, T. J. Shintake, N. J. Shintake

Biochim. Biophys. Acta 1174, 313, 1993
 A:Reference number: S38510; MUID:93385164; PMID:8373812
 A:Contents: annotation; erratum
 C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoprotein reductase; electron transfer; endoplasmic reticulum; FAD; flavoprotein; FMN; NADP; oxidoreductase
 F:79-188/Domain: FMN binding #status predicted <FMN>
 F:80-676/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:82-224/Domain: flavodoxin homology <FLX>
 F:292-326,454-477/Domain: FAD binding #status predicted <FAD>

Query Match 14.0%; Score 761.5; DB 2; Length 678;
 Best Local Similarity 31.9%; Pred. No. 5e-35;
 Matches 208; Conservative 111; Mismatches 269; Indels 65; Gaps 22;

QY 444 FVYAKSKKIP-----LGIPTSPSTEQS-AKVYKKAENANHTPLVLVYSGNMGTAEGR 498
 DB 42 FLFRKKKEEPEFTKISTTTSSVKESSFVKKMKKTGRN-----IIFYGSGTGAEEFAN 96
 QY 499 DLADIAMSKGAPAVATLDH-----AGNLPR-EGAVLTASY-NGHPPDNKQFVDWL 551
 DB 97 RLSDKHRYGMRGMAADPEEYDLADLSLPEIDNLAFCMATYGEEDPTNADQFYDWL 156
 QY 552 DQASDEVKGVYVFGCGDKMATTYQKVP---FIDETLAAGAENIADRGADASDDFEG 611
 DB 157 QETDVL-DLSGVKAVFGLGNKTY-EHNSMGKYVDKLEQAGQRIFFELGDDGDL 214
 QY 612 TYEEMREHMSDVAAVFNLDIENSDNKSTLSLOFVDSADMLAKMH----- 659
 DB 215 DFTITWREQFWPVCHEFVEATGEESIRQYELV---HADTPAKYVTOMGRKSYEN 271
 QY 660 -----GAFSTNVVASKELQPGASRSTRHLEIEL-PKEASYOEGDHLVIRNYEGI 710
 DB 272 QKPPFDANKPFLAATVTRKLNQ-GTERHLMHLELDSDSKIRYESGDHVAVVPANDSNL 330
 QY 711 VNRVTARFG--LDASQOIRLEAEBEKLAHLPLAKTVSEVELLYQVELODPVTRTOLRAMA 768
 DB 331 VNQGLKLGADLVVMSLNINDESNKNGPRPCPTSYRTALTYLDITNP-PRTNVLYEL 389
 QY 769 AKTYCPR-----HKVLEALLEKQAYKEQVLAKRLTMLELLEKYPACENKFSFIALLP 822
 DB 390 AQVASESEBQELHKKMASSGEGKELYLWVVEARRHIALILOYSLRPIIDHLCILLP 449
 QY 823 SIRRYYSISSPPVDEKQASITVSVSGEAMSGYGEYKGIASNYL-AELOEGDT----- 876
 DB 450 RLQARYSIASSKVNHSVHICAVVVEYETKGRIN-KGVAITWMLKPEAPAGEGRAL 508
 QY 877 ITCTISTPOSEFTLPKDPETPLIMVPGTGVAPFRGVQARKOLKEGOSLGEAHLFYGC 936
 DB 509 VPMFVR--KSQFRLPEFKATTPVIMVGPSTGVAFFIGTQERAWLQQGKEVGETLLYYGC 566
 QY 937 RSPHEDLYOELENAQSEGIIT-LHTAFSRMPNQPTVYQVHMEODGKLIIELDQGA 994
 DB 567 RRSDELYREBELAQFHRDGLTQLNVAFSREQAQ-KVYVOHLLKODREHLMKLIHEDGA 625
 QY 995 HFYICGDSQMAPAVEATLTKMSYADVHOVSEADARLMLQOLEKGRYAKDVMA 1047
 DB 626 IYVCGDARNMARDVONTFYDVAELGMEHQAADVYKKLMTKGRISLDVMS 678

RESULT 9

T05582
 NADPH-ferrihemoprotein reductase (EC 1.6.2.4) ATR1 - Arabidopsis thaliana
 N:Alternate names: protein F22K18.280
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002
 C:Accession: T05582; S21530
 R:Bevan, M.; Wedler, H.; Weller, E.; Wambutt, R.; Hohnsels, U.; Mewes, H.W.; Mayer, K.F.J.
 A:Title: The protein sequence database, February 1999
 A:Reference number: T05582
 A:Accession: T05582
 A:Molecule type: DNA
 A:Residues: 1-692 <BEV>
 A:Cross-references: EMBL: AL035356

submitted to the EMBL Data Library, September 1993

A:Description: Isolation and characterization of a cDNA encoding an NADPH-cytochrome P450

A:Reference number: S37159

A:Accession: S37159

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-692 <BEN>

A:Cross-references: EMBL:Z26252; NID:q400531; PIDN:CA61211.1; PID:q400532

C:Superfamily: NADPH-ferrihemoprotein reductase; flavodoxin homology; NADPH-ferrihemoproc

C:Keywords: flavoprotein; NADP; oxidoreductase

F:83-691/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:85-234/Domain: flavodoxin homology <FLX>

Query Match 13.0%; Score 711; DB 2; Length 692;

Best Local Similarity 28.4%; Pred. No. 3.5e-32;

Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

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QY 406 ALHEATVLVGMMLKHPFEDHTNVELDKETTLTKPEGFVYKAKSKIPLGIGPSSTEQ 465
Db 32 ATTSAAVILGLV--FLWRKSPDRSRRLRPVLPK--FTVKHEDDEVV-----76
QY 466 SAKYRKKAENAHNTPLVLVGSNNGTAGSTARDLAD--IMSKGFAPQVATLDSHA---520
Db 77 -----DRGKTKVTFYGTGTGTAEGRKALAEIKARYKAVKVVMDMDYALID 126
QY 521 ----GNLPREGAVLIVTASY-NGHPPDNAKQFVMDLQASADE---VKGVRYSVFGGDX 572
Db 127 DQYBEKLKKEFLVFFMLATYGDGEPTDANARFYKFTGKEERGTLQOLTYGVFALGNR 186
QY 573 NWATTYQKVPFIDETTLAKAENIADRGEADSDDEFGTYEEMREHMSDVAAYFNLDI 632
Db 187 QY-EHFNKIGKIVDEDLTEGGAKRLVPVGLDDQSIDDPNWKETLMPELD---QL 240
QY 633 ENSEDNKSTLSLQFVDSAADMPLA-----KMGAFSTNVAS 669
Db 241 LRDDDDVNTASTPYTAISEYRVVHDPVSPSYENHPNVANGAVFDIHHPCRVNAVR 300
QY 670 KELQPGSARSTRHLEILP-KEASYQEGDHLGVIIRNYEGIVNRVTARFGLDASQIRL 728
Db 301 RELHKPQSDRSCIHIEFPLSGTGYTERGDHGVYAENCDVEEAGKLGOSLDLFLSL 360
QY 729 EAEBEKLAHL-----PLAKTVSVEELLQ-YVELQDPVTRTQLRMAAKTVCPHKVELE 781
Db 361 HTDKEDGSLGSLPPFPGPCTVATLACYADLINPPRKAIVALAHASEPSEAEERLK 420
QY 782 ALLE---KQAYKEQVLAKRLTMLELLEKYPACEMKFSSEFI-ALPSTIRRYYSISSPRV 837
Db 421 FLSSPQGDKEYSKWVGSQRLLEVADPSAKPPLGVFPALIAIRLQPRYYSISSSPRP 480
QY 838 DEKQASITVSVSGEAMSGYGEYKGIASNYLAEL---QEGDTITCFISTPQSEFTLPKD 893
Db 481 APQKVHVTICALVEGPTPG-RHKGVCSVTWMSATPLEKSHDCSRAPFIFIRPSNFKLPAD 539
QY 894 PETPLINVGPGTGAFFRGFVQARKOLKEGOSLGEAHLVFGCSPHEDYLYQEBLENAQ 953
Db 540 HSIPILINVGPGTGLAFFRGFLOERLALKEDEVQLFPALLPFCRRNQMDFIYEDLINNV 599
QY 954 SEGIIIT-LHTAFSPMPNQPKTYVQHVMEQDGLKLELLDQGAHFYICGDSQMAPAVEAT 1012
Db 600 QQGAISELIVAFSR-EGPEKEYQHKMDKAEYLSLISGGYLVCGDAKGMADVARS 658
QY 1013 LMSYADVHVQVSEAD---ARLMLQOLEEKGRAVDW 1046
Db 659 L---HTIVQOQENADSSKAEATVKKLQMDGRYLRDW 692
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Search completed: May 29, 2003, 10:07:19
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 09:55:08 ; Search time 25 Seconds
(Without alignments)
1738.688 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457
Sequence: 1 TTKEMPOKTFGLKNLPL.....RLWLQQLBEKGRYKDVWAG 1048

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	5457	100.0	1048	1	CPXB_BACME
2	3314	60.7	1061	1	CYPD_BACSU
3	3281.5	60.1	1054	1	CYPE_BACSU
4	778.5	14.3	677	1	NCPR_MOUSE
5	777.5	14.2	677	1	NCPR_RAT
6	769	14.1	677	1	NCPR_PIG
7	769	14.1	679	1	NCPR_RABIT
8	767	14.1	676	1	NCPR_HUMAN
9	761.5	14.0	677	1	NCPR_CAVPO
10	735.5	13.5	671	1	NCPR_MUSDO
11	725.5	13.3	679	1	NCPR_DROME
12	723	13.2	601	1	NCPR_SALT
13	721	13.2	690	1	NCPR_PHAU
14	702	12.9	714	1	NCPR_CATRO
15	679.5	12.5	1147	1	NCPR_RAT
16	679	12.4	1429	1	NCPR_MOUSE
17	678	12.4	1429	1	NCPR_RAT
18	675	12.4	1434	1	NCPR_HUMAN
19	671.5	12.3	1147	1	NCPR_HUMAN
20	665.5	12.2	1144	1	NCPR_MOUSE
21	662	12.1	1435	1	NCPR_RABIT
22	661	12.1	1153	1	NCPR_HUMAN
23	655	12.0	1136	1	NCPR_CHICK
24	651.5	11.9	1149	1	NCPR_CAVPO
25	642	11.7	1174	1	NCPR_RHOPR
26	639	11.7	680	1	NCPR_CAVMA
27	614.5	11.3	1247	1	NCPR_ANOST
28	608.5	11.2	1202	1	NCPR_HUMAN
29	602.5	11.0	1204	1	NCPR_BOVIN
30	594.5	10.9	1204	1	NCPR_MOUSE
31	590.5	10.8	1204	1	NCPR_PIG
32	587	10.8	680	1	NCPR_CANTR
33	564.5	10.3	1350	1	NCPR_DROME

34	563	10.3	496	1	NOS2_RABIT	019114 oryctolagus
35	537.5	9.8	678	1	NCPR_SCHPO	P36587 schizosacch
36	534.5	9.8	725	1	MTRR_HUMAN	Q9ubh8 homo sapien
37	522	9.6	690	1	NCPR_YEAST	P16603 saccharomyc
38	518.5	9.5	598	1	CYSJ_ECOLI	P18038 escherichia
39	500.5	9.2	1153	1	NOS2_LYMT	061309 lymanaea sta
40	495.5	9.1	598	1	CYSJ_SALTY	P38039 salmoneella
41	488.5	9.0	601	1	CYSJ_BUCAL	P57503 buchnera ap
42	480.5	8.8	919	1	NOS3_RAT	062600 rattus norv
43	466.5	8.5	682	1	MTRR_CAEEL	017574 caenorhabdi
44	460	8.4	576	1	C972_SOYBN	048921 glycine max
45	459.5	8.4	580	1	C973_ARATH	023365 arabidopsis

ALIGNMENTS

RESULT 1
CPXB_BACME STANDARD; PRT; 1048 AA.
ID CPXB_BACME
AC P14779;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bifunctional P-450:NADPH-P450 reductase (Cytochrome P450 (BM-3))
DE (P450BM-3) [Includes: Cytochrome P450 102 (EC 1.14.14.1); NADPH-
DE cytochrome P450 reductase (EC 1.6.2.4)].
GN CYP102A1 OR CYP102.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89291834; PubMed=2544578;
RA Ruettinger R.T., Wen L.-P., Fulco A.J.;
RT "Coding nucleotide, 5' regulatory, and deduced amino acid sequences
RT of P-450BM-3, a single peptide cytochrome P-450:NADPH-P-450
RT reductase from Bacillus megaterium.";
RL J. Biol. Chem. 264:10987-10995(1989).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=9342510; PubMed=8342039;
RA Boddupalli S.S., Pramanik B.C., Slaughter C.A., Estabrook R.W.,
RA Peterson J.A.;
RT "Patty acid monooxygenation by P450BM-3: product identification and
RT proposed mechanisms for the sequential hydroxylation reactions";
RL Arch. Biochem. Biophys. 292:20-28(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-471.
RX MEDLINE=9342510; PubMed=8342039;
RA Ravichandran K.G., Boddupalli S.S., Hasemann C.A., Peterson J.A.,
RA Daisenhofer J.;
RT "Crystal structure of hemoprotein domain of P450BM-3, a prototype for
RT microsomal P450's.";
RL Science 261:731-736(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-471.
RX MEDLINE=97185914; PubMed=9033595;
RA Li H.Y., Poulos T.L.;
RT "The structure of the cytochrome P450BM-3 haem domain complexed with
RT the fatty acid substrate, palmitoleic acid.";
RL Nat. Struct. Biol. 4:140-146(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.03 ANGSTROMS) OF 1-458 AND 450-649.
RX MEDLINE=9162523; PubMed=10051560;
RA Sevirinouva I.F., Li H., Zhang H., Peterson J.A., Poulos T.L.;
RT "Structure of a cytochrome P450-redox partner electron-transfer
RT complex.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1863-1868(1999).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 1-470.
RX MEDLINE=21552924; PubMed=11695892;
RA Haines D.C., Tomchick D.R., Machius M., Peterson J.A.;

RT "Pivotal role of water in the mechanism of P450BM-3.";
 RL Biochemistry 40:13456-13465(2001).
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. CATALYZES
 CC HYDROXYLATION OF MEDIUM AND LONG-CHAIN FATTY ACIDS AT OMEGA-1,
 CC OMEGA-2 AND OMEGA-3 POSITIONS. WITH OPTIMUM CHAIN LENGTHS OF 14-16
 CC CARBONS (LAURIC, MYRISTIC, AND PALMITIC ACIDS). THE REDUCTASE
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
 CC P450.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferriocytocrome.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
 CC P450 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL, U04832; AA87602.1; -.
 DR PIR; A34286; A34286.
 DR PDB; 2HPD; 31-OCT-93.
 DR PDB; 2BMH; 31-JUL-94.
 DR PDB; 1FAG; 12-FEB-97.
 DR PDB; 1FAH; 12-FEB-97.
 DR PDB; 1BU7; 23-SEP-96.
 DR PDB; 1BVY; 23-FEB-99.
 DR PDB; 1JPZ; 09-NOV-01.
 DR InterPro; IPR001128; Cytochrome P450.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001709; FPN_cyt_reductase.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00067; P450; 1.
 DR Pfam; PF00175; NAD binding; 1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00667; FAD binding; 1.
 DR PRINTS; PR00371; FENCR.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; 1.
 KM Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KM Multifunctional enzyme; FMN; FAD; Flavoprotein; 3D-structure; NADP.
 FT INT_MET 0 0
 FT DOMAIN 1 471
 FT BINDING 472 1048
 FT BINDING 400 400
 FT TURN 12 13
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 FT TURN 109 111
 FT HELIX 112 131
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 FT TURN 135 136
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 FT HELIX 141 158
 CYTOCHROME P450.
 NADPH-P-450 REDUCTASE.
 HEME.

FT HELIX 164 166
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 FT TURN 445 450
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Query Match 100.0%; Score 5457; DB 1; Length 1048;
 Best Local Similarity 100.0%; Pred. No. 98-298;
 Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIKEMPOKTFGEIKMLPLINTDKPVQALMKIADIEGEIFKFPAGRVTRYLSSQRLIKE 60
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 DB 61 ACDBSRFDKLSQALKFVRFPADGGLFTSWTHKMKKANNILLPSSQAMGYHAMV 120
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 DB 121 DIAVOLQKMERLNADHEIEVPEDMTRLTDTGLGCFNRFNSFYADOPHPTTSWRA 180
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 DB 181 LDEAMNKLQRANPDPAVDENKRFQEDIKVNDLVYDKIADRKASGEQSDLLTHMLNG 240
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 DB 241 KDPETGEPDLDENIRYOITFLIAGHETTSGLSPALYFLVKNPHYLQKAABEARLVLD 300
 QY 301 PVPSTYKOVKOLKYVGMVLANBALRLMTPAPAFSLYAKEDTVLAGEEYPLEKDELMVLIPOL 360
 DB 301 PVPSTYKOVKOLKYVGMVLANBALRLMTPAPAFSLYAKEDTVLAGEEYPLEKDELMVLIPOL 360
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 DB 361 HRDKTIWGDVVEEFRRPFENPSAIPQAHKPFNGGRACITGGQFALHEATLVLGMMVKH 420
 QY 421 FDEBDHTNYELDIKETITLKPBGFVYAKSKKIPLGIGPSPSTBQSAKKYRKQAEANANT 480
 DB 421 FDEBDHTNYELDIKETITLKPBGFVYAKSKKIPLGIGPSPSTBQSAKKYRKQAEANANT 480

Db 421 FDEEDHTNVELDKETITLTKEPFGVAKAKKIPLGCIPEBPSTEQSKKVKRKAENAHNT 480
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 Db 481 PLLVLVSGNMGTAEGTARDIADAMSKGAPQVATLDSHAGNLPREGAVLITVASYNGHP 540
 QY 541 PDNAKQFVMDLDAQSADEVKGVYVSGCGDKRWATTYQVPAVIDETTLAKAGENIADR 600
 Db 541 PDNAKQFVMDLDAQSADEVKGVYVSGCGDKRWATTYQVPAVIDETTLAKAGENIADR 600
 QY 601 GEADASDEPGEYBEMREHMSDVAAAFNLDIENSBNKSTLSIQFVDSAADPMLAMHG 660
 Db 601 GEADASDEPGEYBEMREHMSDVAAAFNLDIENSBNKSTLSIQFVDSAADPMLAMHG 660
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 Db 661 AFSTNVASKELOOPGASARSTRHELELPKASAYOEQDHLGVIPRNEGIVNRVTAFCGL 720
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 Db 721 DASQOIRLEAEERKLAHLPLAKTVSVBELLYVELQDPVTRTOLRMAAAKTCPPHKEVL 780
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 Db 781 EALLEKQAYKEOVLAKRLTMLELEKYPACEMKSEFIALPSTRPRYSSISSPRVDEK 840
 QY 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEDTTCFISTPQSEFTLPKDPETPLIM 900
 Db 841 QASITVSVSGEAMSGYGEYKGIASNYLAELQEDTTCFISTPQSEFTLPKDPETPLIM 900
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 Db 1021 HQVSEADARLMLQOLEKGRYAKDVWAG 1048
 RESULT 2
 ID CYPD_BACSU STANDARD; PRT: 1061 AA.
 AC 008334;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable bifunctional P-450:NADPH-P450 reductase 1 [Includes:
 DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
 DE (EC 1.6.2.4)].
 GN CYPD OR CYP102A2.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97453479; PubMed=9308178;
 RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
 RA Duesterhoeft A., Ehrlich S.D.;
 RT "Sequence of the Bacillus subtilis genome region in the vicinity of
 RT the lev operon reveals two new extracytoplasmic function RNA
 RT polymerase sigma factors Sigv and Sigz.";
 RL microbiology 143:2939-2943(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berteiro M.G., Bessieres P., Bolotin A., Borchert S.,

RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell I.B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Denicot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
 RA Gilm S.Y., Glaeser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Galspeli G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaer-Bianchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kunano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Maesuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portollik S., Prescott A.M.,
 RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scotfone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Toomari A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzmeger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
 CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
 CC P450 (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferri-cytochrome = NADP(+) + 2
 CC ferri-cytochrome.
 CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.
 CC -1- COFACTOR: FAD AND FMN (BY SIMILARITY).
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE CYTOCHROME
 CC P450 FAMILY.
 CC
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 CC
 CC EMBL: D87979; BAA20123.1; -
 CC HSSP: 299107; CABI2544.1; -
 CC HSSP: P14779; 1JPZ.
 CC
 CC Subtilisin, BGI2871; CYPD.
 CC InterPro: IPR001128; Cytochrome_P450.
 CC InterPro: IPR003097; FAD_binding.
 CC InterPro: IPR001709; FMN_cyt_reductase.
 CC InterPro: IPR001226; Flavodoxin.
 CC InterPro: IPR001433; Oxred_FAD/NAD(P).
 CC Pfam: PF00067; P450; 1.
 CC Pfam: PF00175; NAD_binding; 1.
 CC Pfam: PF00258; Flavodoxin; 1.
 CC Pfam: PF00667; FAD_binding; 1.
 CC PRINTS: PR00371; PFNCR.
 CC PRINTS: PR00385; P450.
 CC PROSITE: PS00086; CYTOCHROME_P450; 1.
 CC Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 CC Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
 CC Complete proteome.
 CC DOMAIN 1 474 CYTOCHROME P450.
 CC FT DOMAIN 475 1061 NADPH-P-450 REDUCTASE.
 CC FT BINDING 403 403 HEME (BY SIMILARITY).
 CC SEQUENCE 1061 AA; 119467 MW; 7915DACC20578978 CRC64;
 Query Match 60.7%; Score 3314; DB 1; Length 1061;

Beet Local Similarity 59.5%; Pred. No. 7,1e-178; Indels 12; Gaps 6;
Matches 628; Conservative 156; Mismatches 259;

5 MPOEFTFELKMLPLNTDKPVALMIADEIGEFKFEAPGRVTRYSORLIKEACDE 64
7 IPOEFTFELKMLPLNTDKPVALMIADEIGEFKFEAPGRVTRYSORLIKEACDE 66
65 SRPDKNSQALKFVNDPAGDGLFTSWTEHKWKKAHNLLPSQOAMKGYHAMVDAV 124
67 ERPFKISGALKFKVAFSGDGLFTSWTEHKWKKAHNLLPSQOAMKGYHAMVDAV 126
125 QLVQKWEKNADENHEVEDMTRLLDTIGCGFVYRNSYRROPHFIFISMRALDEA 184
127 QLVQKWEKNADENHEVEDMTRLLDTIGCGFVYRNSYRROPHFIFISMRALDEA 186
185 MNKLQRPADDPAYDENROFOEDIKVANDVDKIIADKKSGEOD-DLTHMLNGKPD 243
187 MHQWQRLDVQDKLWRTKQFRYDQTMFSLVDSIIARRANGODEDKLARKMLNVEDP 246
244 ETGEPLDENIRYQITITFLIAGHETTSGLSPALYFLVKNPHVLOKAAEABARVLDPEP 303
247 ETGEPLDENIRYQITITFLIAGHETTSGLSPALYFLVKNPHVLOKAAEABARVLDPEP 306
304 SYKQVQKQYVGMVLENLRLMPRPAISLAKEDTVLGSEYPLEKGBELWVLLPOLHRD 363
307 TYKQVLELTYIRMLNESLRLMPRPAISLAKEDTVLGSEYPLEKGBELWVLLPOLHRD 366
364 KTIWGDVVEERPERFENPASAIPQAFKPFNGGACIGQOFAHLEATLVGMMLKHPDF 423
367 RDAWKGAAEERPERFENPASAIPQAFKPFNGGACIGQOFAHLEATLVGMMLKHPDF 426
424 EDHTNVELDIKETTLLKPEGVVAKSKKIPGLGIPSPSTQSA--KVKRKAENA-- 477
427 IDHENEYEDIDIKETTLLKPEGVVAKSKKIPGLGIPSPSTQSA--KVKRKAENA-- 486
478 --HNTPLVLYGSMNGTAEGRADLADLANSKGFAPQATLDHAGNLPREGAVITVVAS 535
487 GLNNRPLVLYGSDGTAGVARELADLANSKGFAPQATLDHAGNLPREGAVITVVAS 546
536 YNGHPDPAKQFVMDLQASADEVGVAVSVFGCGDKMATTYQKVPADITETLAKGAE 595
547 YNGRPSNAGQFVMDLQASADEVGVAVSVFGCGDKMATTYQKVPADITETLAKGAE 606
596 NIADGEGADSDDEPGTYEERREHMSDVAAVFNLDI-ENSEDNKSTLSIQFVDSADMP 654
607 RFSARGEGEDVSGDEGQLDDEWKKSWADAIKAFGLLELNENDKERSSTLSIQFVDSADMP 666
655 LAKHGAFTNVASKEIQPGSASTRHLEILPKESYQEGDHLGVTPNNYEGIVNRV 714
667 LARSYEASHASIAERRELQASDSSTHIEIALPPDVEYQEGDHLGVTPNNYEGIVNRV 726
715 TARFGLDASQOIRLEAEBEKLAHLPLAKTVSEVELLOY-VELQDPVTRTOLRAMAKVVC 773
727 LHRGRLKKTDOVTLSSASGRSAGHPLRGFVSLHDLTSVSEVQEAATAQIRELASFVVC 786
774 PPHKVELEALLEKQAYKEQVLAKRLTMLLEKTPACEMKSEFIALPSIRPRYSISS 833
787 PPHRELELELAEQVYQEQILKKRISMULDLEKTYACAMPFERFELRLPKPRYSSISS 846
834 SPRVDEKASTTVSVSEAMSGVGEYKIGINSNYIAELQEBDTITCFISTQSEFTLPKD 893
847 SPRVPRQASTTVGVRRPAMSGREYKGVASNDIAEQADDVMTFRTESESRQOLTKD 906
894 PETPLIMVGPSTGVAPFRGFVQARQOLKEQOSGLAEHALYFGCRSPHEDVYOELENAQ 953
907 PETPLIMVGPSTGVAPFRGFVQARQOLKEQOSGLAEHALYFGCRSPHEDVYOELENAQ 965
954 SEGIITLHTAFSRMNPQKTYVQVHVMEDQKLLIELDQGAHFYICGDSQMAPVEATL 1013
966 KDGIATVHTAFSRMNPQKTYVQVHVMEDQKLLIELDQGAHFYICGDSQMAPVEATL 1025
1014 MKSYADVHTAFSRMNPQKTYVQVHVMEDQKLLIELDQGAHFYICGDSQMAPVEATL 1048

DB 1026 QKAYQAVHGTGEQBAQWMLHLDOTGMVADVMAG 1060

RESULT 3
CYPE_BACSU
ID CYPE_BACSU STANDARD; PRT; 1054 AA.

AC 008336;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable bifunctional P-450:NADPH-P450 reductase 2 (Includes:
DE Cytochrome P450 102 (EC 1.14.14.1); NADPH-cytochrome P450 reductase
DE (EC 1.6.2.4)).
GN CYPE OR CYP102A3.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:168;
RX MEDLINE=97453479; PubMed=9308178;
RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
RA Duesterhoeft A., Ehrlich S.D.;
RT "Sequence of the Bacillus subtilis genome region in the vicinity of
RT the lev operon reveals two new extracytoplasmic function RNA
RL polymerase sigma factors Sigv and Sigz.";
RM Microbiology 143:2939-2943 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN:168;
RX MEDLINE=96044033; PubMed=9384377;
RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Britnell S.C., Bron S.,
RA Brouiller S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel P.A.,
RA Demizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haeck J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Katamata D., Kasaahara Y., Klaert-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogsh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Patro V., Pohl T.M., Portetelle D., Portwollik S., Prescott A.M.,
RA Priesecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
RA Seliguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,
RA Viari A., Wambut R., Wedler E., Wedler H., Weitenegger T.,
RA Witters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -I- FUNCTION: FUNCTIONS AS A FATTY ACID MONOOXYGENASE. THE REDUCTASE
CC DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME
CC P450 (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferricytochrome.
CC -I- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC oxidized flavoprotein + H(2)O.
CC -I- COFACTOR: FAD AND FMN (BY SIMILARITY).
CC -I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.

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DR EMBL; U93874; AAB80867.1; -;
DR EMBL; Z99117; CAB14658.1; -;
DR HSSP; P14779; 1JPZ.
DR Subtilisin; BGL2299; cyte.
DR Interpro; IPR001128; Cytochrome_P450.
DR Interpro; IPR003097; FAD_Binding.
DR Interpro; IPR001709; FPN_Cyt_redctase.
DR Interpro; IPR001226; Flavodoxin.
DR Interpro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00067; P450; 1.
DR Pfam; PF00175; NAD_Binding; 1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00667; FAD_Binding; 1.
DR PRINTS; PR00371; FPNCR.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP;
KW Complete proteome.
FT DOMAIN 1 475 CYTOCHROME P450.
FT BINDING 403 403 NADPH-P-450 REDUCTASE.
FT BINDING 403 403 HEME (BY SIMILARITY).
SQ SEQUENCE 1054 AA; 118675 MW; 705F8E27866CA110 CRC64;

Query Match Best Local Similarity 58.5%; Pred. No. 4.6e-176; Length 1054;
Matches 614; Conservative 173; Mismatches 254; Indels 9; Gaps 6;

QY 5 MPDPTFGLKLNPLNTDKPVQALMKIADLGEIFKFEAPGRVTRYLSORLIKEACDE 64
DB 7 IPEKTYGKPLNPLHLEKEQLSGSLMRLADELPFDFPGVSVFSGHNLVAEVCDE 66
QY 65 SRPKNLSQLKPYRDRAGSLFTSMHEKWKKAHMLLPSEFOQAMKGYHAMVUAV 124
DB 67 KRFENKLGKGLQKREFGDELFTSWHEPWOQKAHMLLPSEFOQAMKGYHAMVUAV 126
QY 125 QLVQKMERLNADDEIEVEDMTRLTLDTLIGLGFENFNSFYRQPHPTISWRAUDEA 184
DB 127 QLVQKMERLNADDEIEVEDMTRLTLDTLIGLGFENFNSFYRQPHPTISWRAUDEA 186
QY 185 MNKLQANPDDPAYDENKROFOEDIKYMNLDLVKIIADRKASGEQS--DDLTLHMLGKDP 243
DB 187 MNQSKRLGLQDKMVKTLQFOKOIEVNSLVDMIAERKANPDENIKDLTLMLVAKDP 246
QY 244 EFGEPDLDDENIRYQITFLINAGHTTSGLSFALYFLVKPNHVLQKAEEAARLVUPVP 303
DB 247 VTGGLDDENIRYQITFLINAGHTTSGLSFALYFLVKPNHVLQKAEEAARLVUPVP 306
QY 304 SYKQVKQKYGWNLNEALRLMPAPAFSLYAKEDTVLGGEPLEKDELMVLIPLQHRD 363
DB 307 EYKQIQKIKRMLNLTETRLRYTAPAFSLYAKEDTVLGGEPLEKDELMVLIPLQHRD 366
QY 364 KTIWGDDVEERPRFENPSAIPQAFKPFNGORACIGQOFALHEATLVLMMLKHEDF 423
DB 367 QNANGPDAEDPRFEDPSSIPHHAYKPFNGORACIGQOFALHEATLVLMMLKHEDF 426
QY 424 EDHTNYELDIKETITLPRGEGVYAKAKKIPLGIGIPSESTQS--AKYRKKAKENAHNT 480
DB 427 INHTGYELKIKETITLPRGEGVYAKAKKIPLGIGIPSESTQS--AKYRKKAKENAHNT 484
QY 481 PLVLYSGNMGTAGTARGLDILMNSKGFAPQVATLDSHAGNLPRGAVLIVTSYNGHP 540
DB 485 PLVLYSGNMGTAGTARGLDILMNSKGFAPQVATLDSHAGNLPRGAVLIVTSYNGHP 544
QY 541 PDNAKQFVDWLDQASADEVKGRYSVFQCGDKMAITYYQKVPAPIDETTLAKGAENIADR 600

DB 545 PDNAKQFVDWLDQASADEVKGRYSVFQCGDKMAITYYQKVPAPIDETTLAKGAENIADR 604
QY 601 GADADDEEGYEEWREHMSDVAAVFNIDENSENSTLSLQFVDSAADPMLAKMG 660
DB 605 GEDDADDEESRESSENNFWKETMAFPINELAQKEDPSSLITLSLETETEPVAKAG 664
QY 661 AESTNVASKELOQPSARSTRHLEIEPKASVQEGDHLGVIPNNYEGIVNRVAFGL 720
DB 665 AFGIYLERNELOTAASTRSTHIEIEIPAGKYKEGDHIGILPKNSRELIVORVLSRFGI 724
QY 721 DASQIRLAEAEKLANHPLAKTVSEELL-QYVELQDPTVTRQAPAMAKTCEPHKYE 779
DB 725 QSNHVIKVSASAH-MHLPMDRPIKAVDLSSVVELQEPASRLQCELASVYVCPHQYE 783
QY 780 LEALTEKQA-YKEQVLAKEITLMLELEKYPACEMKSEETALLPSIRPYVSISSSPRYD 838
DB 784 LEOVLVDDGITYEQVLAKEITLMLELEKYPACEMKSEETALLPSIRPYVSISSSPRYD 843
QY 839 EKQASITVSVSGEAMSGYGEYKGLASNYLAIEQEGDTTCFISTPQSEFTLPKDETPU 898
DB 844 ANIVSWTVGVKVASASMSGGEYGVASNYLAIEQEGDTTCFISTPQSEFTLPKDETPU 903
QY 899 IMVGETGVAPPRGFYQARKOLKEQOSLGEALHYEGCSPHEDYLYOELNAQSEGI 958
DB 904 IMVGETGVAPPRGFYQARKOLKEQOSLGEALHYEGCSPHEDYLYOELNAQSEGI 963
QY 959 TLHTASRMDNPQKTYVQVHMEODGKLLLELDQGANFYICGDSQMAVAVENTLKSVA 1018
DB 964 TIRCRSRVENEKGVQVHLKODTQKMLTLIEKGNHYVCGDSQMAVAVENTLKSVA 1023
QY 1019 DVHQSADARLWLQLEBKGRYAKDVWAG 1048
DB 1024 ABRKASQESASVWLQKLDQORRYKDVWAG 1053

RESULT 4
NCPR MOUSE STANDARD; PRT; 677 AA.
AC P37040;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ddv;
RX MEDLINE=94281246; PubMed=8011664;
RA Ohtsuka S., Ishizaki K., Kametaki T., Shiraki N.;
RT "Mouse NADPH-cytochrome P-450 oxidoreductase: molecular cloning and
functional expression in yeast."
RL Biochim. Biophys. Acta 1186:137-141(1994).
CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
ferricytochrome.
CC -!- COFACTOR: FAD AND FMN.
CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
BR MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
REDUCTASE.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D17571; BAA04496.1; -.
DR HSSP; P00388; IAMO.
DR SWISS-2DPAGE; P37040; MOUSE.
DR MGI; MGI:97744; Por.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001709; FPN_cyt_reductse.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00175; NAD_binding_1.
DR Pfam; PF00258; Flavodoxin; 1.
DR Pfam; PF00667; FAD binding; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
DR Membrane; Acetylation.
DR MOD_RES; 0 BY SIMILARITY.
FT INIT MET 0 ACETYLATION (BY SIMILARITY).
FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 624 640 NADP (ADP PART) (BY SIMILARITY).
SQ SEQUENCE 677 AA; 76912 MW; 00655C14D0E1C5E9F CAC64;

Query Match 14.3%; Score 778.5; DB 1; Length 677;
Best Local Similarity 32.3%; Pred. No. 2.6e-36;
Matches 212; Conservative 106; Mismatches 267; Indels 71; Gaps 22;

QY 444 FVFAKSKKIP-----LGGIPSPSTEQS-AKVKRKAENAHNTPLVLYGSMGAEGRAR 498
DB 41 FIFKKKEEIEPFESKIQTTAPVKESSVEKMKTKGRN-----IIVFGSGTGAEEFAN 95
QY 499 DLADIAMSKGPAQVATLDSH-----AGNLPR-EGAVLITVASY-NGHPDNNAQFVWML 551
DB 96 RLSDAHRVYGMKGSADPEEYDLADLSLPEIDSLVFCMATGEGPPTNADQFYVWL 155
QY 552 DQASADEKVRVYFGCGDKMATTVQKVA--FIDETLAAGAENIADRGEDASDD 608
DB 156 QETDVD-LTVGVFAVFGIGNK---TYEHFNMGKYVDQRLQEOGAQRIFELGLDDGN 210
QY 609 FEGTYEERHEHMSVNAFYNLDIENSEDNKSTSLQVDSAAAPLAKMH----- 659
DB 211 LEEPFITRKEQFWPAVCEFFGEVATGESSIRQYELVNH---DMDTAKVITGEMGRUKS 267
QY 660 -----GAFSTNVASKELQPGSASSTRHLEIEL-PKEASYOEGDHLGIVPRNY 707
DB 268 YENQKRPEDAKNPFLAATTRKNQ--GTERHMLHLEIDSKIRYSGDHVAVYPRND 326
QY 708 EGIYNRVTAARG--LDASQQLRLAEERKLAHLPLAKTVSVEBLQYVELDDPYTRIOLR 765
DB 327 STLVAQGEIIGADLDVIMSLNLDSEENKNGPPECPFTYATLYADITNP-PRIVVL 385
QY 766 AMAAKTVCP-----HKVELLEALKEQAYKEOVLAKLTMLELLEKYPACEMKPFSEIA 819
DB 386 YELQVYSEPEQEHLMFASSSGEGKELYLSVVEARRHLALITQDPSPRPPIDLCE 445
QY 820 LLPISIRPRVYSSISPRVDEKQASITVSVSGEAMSGYGEKGIASNYL-----AEIQE 873
DB 446 LLPLQLAYVYSSISKXVHNSVHICAVAVEAKSGVNV-KGVALTSLRLRKEPAGENG 504
QY 874 GDITTCFSTQSEETLEPKDETPYLIMGEGTGAFFGFLVQARKQLKEGQSGISEAHLY 933
DB 505 RALVPMFVR--KSFRLPFPKPTPIVWGPETGVAFFGFLQERAMLEEGKEVGETILY 562
QY 934 FGCRSPHEDYLYOELENAQSEGIT-LHTAFSRNPQPKTYOVHVMQDQKLIIEILDQ 992
DB 563 YGCRSDEDDYLYREELAFHKGALTLQNVAFSR-EQAHKYVVOHLRKHSHMLKLIHE 621

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QY 993 -GAHFYICGDSQMAPAVEATLTKSYADVHQSSEADARLMLQOLEEKGRYAKVWA 1047
DB 622 GAAHYVCGDARRMAKXQVNTFYDIVAEFGPMETHQAVDVYKXKLMTGRYSLDVWS 677

RESULT 5
NCPR RAT ID NCPR RAT STANDARD; PRT; 677 AA.
AC P00388;
DT 21-JUN-1986 (Rel. 01, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-JUN-2002 (Rel. 41, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN POR.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140278; PubMed=3919392;
RA Porter T.D., Kasper C.B.;
RT "Coding nucleotide sequence of rat NADPH-cytochrome P-450
RL oxidoreductase cDNA and identification of flavin-binding domains.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86163762; PubMed=3082610;
RA Murakami H., Yabuaki Y., Ohkawa H.;
RT "Expression of rat NADPH-cytochrome P-450 reductase cDNA in
RL Saccharomyces cerevisiae.";
RN [3]
RP SEQUENCE OF 413-677 FROM N.A.
RX SPRAIN-Mistat; TISSUE=Liver;
RL MEDLINE=9104888; PubMed=2125483;
RA Porter T.D., Beck T.W., Kasper C.B.;
RT "NADPH-cytochrome P-450 oxidoreductase gene organization correlates
RL with structural domains of the protein.";
RN [4]
RP Biochemistry 29:9814-9818(1990).
X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97385116; PubMed=9237990;
RA Wang M., Roberts D.L., Paschke R., Shea T.M., Masters B.S.S.,
RL Kim J.-J. P.;
RT "Three-dimensional structure of NADPH-cytochrome P450 reductase:
RL prototype for FMN- and FAD-containing enzymes.";
RN [5]
RP Proc. Natl. Acad. Sci. U.S.A. 94:8411-8416(1997).
X-RAY CRYSTALLOGRAPHY (1.80 ANGSTROMS) OF MUTANTS.
RX MEDLINE=2136908; PubMed=11371558;
RA Hubbard P.A., Shen A.L., Paschke R., Kasper C.B., Kim J.-J. P.;
RT "NADPH-cytochrome P450 oxidoreductase. Structural basis for hydride
RL and electron transfer.";
RN J. Biol. Chem. 276:29163-29170(2001).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferricytochrome.
CC -1- COFACTOR: FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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DR Pfam: PF00258; flavodoxin. 1.
 DR Pfam: PF00657; FAD_binding. 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KM Membrane; Acetylation.
 FT MOD_RES 72 ACETYLATION.
 FT NE_BIND 171 FMN (PYRIDINE PART) (BY SIMILARITY).
 FT NE_BIND 315 326 FAD (ADP PART) (BY SIMILARITY).
 FT NE_BIND 452 462 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NE_BIND 530 548 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NE_BIND 625 641 NADP (ADP PART) (BY SIMILARITY).
 FT CONFLICT 40 41 YW -> NY (IN REF. 2).
 FT CONFLICT 53 53 E -> N (IN REF. 2).
 FT SEQUENCE 679 AA; 7658 MW; B1A163FA53A5988B CRC64;
 Query Match 14.1%; Score 769; DB 1; Length 679;
 Best Local Similarity 31.7%; Pred. No. 8.9e-35; Indels 96; Gaps 24;
 Matches 212; Conservative 111; Mismatches 250;
 QY 444 FVYKAKSKIP-----LGIPSPSTQGA--KVKAKKAKNAHNTPLVLVYSGNMGTAEGTA 497
 DB 42 FLRRKKKEVEPEFKIQAPTSSSYKSSFYKMKKTGRN-----IVFYSGQTAEFA 96
 QY 498 RDLADLAMSGRFAPQVATLDSH---AGNIPREGAVLIV--TASY-NGAPPDNAKQFVDW 550
 DB 97 NRSLSKDAHRYGKMGMAADPEEYDLADLSLPEINNALAVFCMATYVGGEDPTDAQDFYDW 156
 QY 551 LDQASDEVGVYVYVSGCGDKMATTYQKVPV---FIDETLAKGKEMNADGEADASD 607
 DB 157 LGETDWD-LSGVKKVAVGLNKK---YVERFNMAKGVDRLEQLGQRIFFELGMDDA 211
 QY 608 DPEGTVEEMHNSDVAAVFNLDIENEDNKSTLSQFVDSADAMPLAMH----- 659
 DB 212 NLEDEFTWMEQWPAVCEHFGVATGESSIQYELVL---HTDIDVAVYGGEMRLK 268
 QY 660 -----GAFSTNVVASKELQOPGASRSTRHLEIL-PKEASYOGDHLGVIPRN 706
 DB 269 SYENOKPEPDANKPFLATVTNTRKLNQ-GTERHLMHLELIDISDKIRYESGDHVAVYPAN 327
 QY 707 YEGIVRVTRFGLDASQOI---RLEAEERKLAHLPL-----AKVSV 746
 DB 328 DSAIVNQLGEITLGDLDVVSINLNDSESKKHPFPPTSYRTALTYLDTNPPRTNVL 387
 QY 747 EELLQVVELQDPVTRQLRAMAAKTVPKPKVELEALLKQAVYKEOYLAKRLTWLELLEK 806
 DB 388 YELAQYA--ADPAQEBQLKMASSSG-----EGKELVLSWVEARRHIALILOD 434
 QY 807 YPACEMKFEFFIALLPISIRPVYSSISSPVNDEKASITVSVSGEAMSGYGEYKGIASN 866
 DB 435 YPGLRPPIIDLCELPRLQARYSIASSSKVHPNSVHICAVAVEYETKARLN-KGVATS 493
 QY 867 YL-AELOEDPT-----ITCFISTPQSEFTLPKDEFTLWVGRTGYAPRGRVQARKQ 920
 DB 494 WLAKKPEAGNGRALTVMFVR--KSGFRLPFKATTVIVWGPOTGAIPGFOEAWL 551
 QY 921 KEQGOSLGEHLYFGCSPHEDLYOEBELNAOSEGIT--LHTAFSMPQPKTYVOHW 979
 DB 552 RQGGKEVGETLYYCGRAEDVLYREELGPOKQDGLSOLNNAFSEQAO-KYIVQHL 610
 QY 980 EODGKULIELLD-GAHFYICGDSQONAPAVEATLMKSYADVHGVSEADARLMLOOLEEK 1038
 DB 611 RRDKEHLMRLIHGGAHIVYCGDARNMARVQNTFYDIVALGMEHAQAVDYVKLMTK 670
 QY 1039 GRAYADYWA 1047
 DB 671 GRYSLDVWS 679

DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
 GN POR OR CYPR.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90105390; PubMed=2513880;
 RA Hanin M., McManus M.E., Birkett D.J., Lee T.D., Shively J.E.;
 RT "Structural and functional analysis of NADPH-cytochrome P-450
 RT reductase from human liver: complete sequence of human enzyme and
 RT NADPH-binding sites.";
 RL Biochemistry 28:8639-8645(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92198003; PubMed=1550342;
 RA Shepard E.A., Palmer C.N., Segall H.J., Phillips I.R.;
 RT "Quantification of cytochrome P450 reductase gene expression in human
 RT tissues.";
 RL Arch. Biochem. Biophys. 294:168-172(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Czerwikowski M., Sahni M., Madan A., Parkinson A.;
 RT "Polymorphism of human CYPOR: expression of new allele.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Murakami H.O., Ogawa H., Nisimoto Y.;
 RT "cDNA cloning and characterization of NADPH-cytochrome P-450 reductase
 RT in human HL-60 cells.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 61-241.
 RX MEDLINE=99156068; PubMed=10048323;
 RA Zhao Q., Modi S., Smith G., Paine M., McDonagh P.D., Wolf C.R.,
 RA Tew D., Lian L.Y., Roberts G.C., Driessen H.P.;
 RT "Crystal structure of the FMN-binding domain of human cytochrome P450
 RT reductase at 1.93 A resolution.";
 RL Protein Sci. 8:298-306(1999).
 CC -!- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -!- CATALYTIC ACTIVITY: NADPH + 2 ferri-cytochrome = NADP(+) + 2
 CC ferri-cytochrome.
 CC -!- COFACTOR: FAD AND FMN.
 CC -!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -!- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
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 CC EMBL; S90469; AAB21814.1; -
 DR EMBL; AF258341; AAG09798.1; -
 DR EMBL; AB051763; BAB18572.1; -
 DR PIR; A33421; A33421
 DR PDB; 1BIC; 24-NOV-99.
 DR Genew; HGNC:9208; POR.
 DR MIM; 124015; -

DR InterPro: IPR003097; FAD_binding.
 DR InterPro: IPR001709; FPN_cyt_redctse.
 DR InterPro: IPR001094; Flavodoxin like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00175; NAD_binding_1.
 DR Pfam: PF00258; Flavodoxin; 1.
 DR Pfam: PF00667; FAD_binding; 1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KM Membrane; Acetylation; Polymorphism; 3D-structure.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 528 546 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 622 638 NADP (ADP PART) (BY SIMILARITY).
 FT VARIANT 499 499 A -> V.
 FT VARIANT 550 550 /FTID=VAR_004617.
 FT VARIANT 550 550 R -> Q.
 FT CONFLICT 404 404 M -> L (IN REF. 4).
 FT CONFLICT 517 517 F -> L (IN REF. 2 AND 4).
 FT CONFLICT 536 537 VA -> WH (IN REF. 2).
 SQ SEQUENCE 676 AA; 76558 MM; 883EA13797020D70 CRC64;
 Query March 14.1%; Score 767; DB 1; Length 676;
 Best Local Similarity 32.4%; Pred. No. 1.1e-35;
 Matches 211; Conservative 113; Mismatches 264; Indels 64; Gaps 23;
 QY 444 FVYAKSKLP---LGGIPSPSTEOS-AKVRKKAEMAHNTPLVLGSMNGTAEGTAR 498
 DQ 41 FLFKKKKEVEEFKIQTLTSSVRESSFVEKMKTKGRN---IIVFGSGTGAEEFAN 95
 QY 499 DLADIANSKGPAPVATIDSH---AGNLPREGAVLY--TASY-NGHPNNAKQPDWL 551
 DQ 96 RLSDARHYGKRGMSADPEEYDLADLSLPIDNALVFCVATYGEQDPTNADDFYDWL 155
 QY 552 DQASADEKGVRYVFGGCDGNWATTYOKVPA---FIDEPLAAGAENIADRGESDSD 608
 DQ 156 QETVVD-LSGVKVAFGLGNK---TYEHFAMGKYVDKRLQJGAKRIFELGLGDDGN 210
 QY 609 FEETYEEMREHMSDVAAYFNLDIENSSEDKSTLSLOP---VDSA---ADMPLAKM-- 659
 DQ 211 LEEDFITMREGFPAVCEHFEVATGESSIRQYVELVHTDIDAKYVMGMSGLKSYEN 270
 QY 660 -----GASTNVVASKELQPGSASTHLEIEL-PKASIOEGDHLGVIPRYEGI 710
 DQ 271 QKPEFDANKPFLAVTTNRKLNQ-GTERHMLHLEIDISDKIRYESGDHVAVYPAWSAL 329
 QY 711 VNRVYARFG--LDASQOIRLEAEFEKLAHLPLAKTVSEELQVVELQVLODPVTRQLRMA 768
 DQ 330 VNOGKILGADLDVYMSLNLIDESNNKHPPTSTRTALTYYIDINP-PRINVLVEL 388
 QY 769 AKTVCPPHKVELLEALL------KQAYKEQVLAIRLTMLELLEKYPACEMKFSFIALP 822
 DQ 389 AQVASEPEQGLLRKMASSGEGKELVSWVEARHILALLOCPSPRIPIIDHCELLP 448
 QY 823 SIRPRYISISSPRVDEKQASITVSVSGEAMSGYGEKGIASNYL-AELOEGDT----- 876
 DQ 449 RLQARYSIASSSKVHPNSVHICAVVVEYETKAGIN-KGVATWMLRAKEPAGENGGRAL 507
 QY 877 ITCISTPQSEFTLPKDEPTLIMWGPEGTGAPRPGFQAKQKQEGOSIGEAHLVRC 936
 DQ 508 VPMFVR-KSQFRLPFKATPVLIMWPGTGAAPFGIGQERAMWQOQKEVETLLYYGC 565
 QY 937 RSPHEDLYQEELENAOSEGIT--LHTAFSRMPNPKTYVOHWMEODSKLIELLDQAH 995
 DQ 566 RRSBEDYVIRELMAQFHRDGLTQUNVAFSRQSH-KYYVGHLLKQDEHMKLIEGGAH 624
 QY 996 FYICGDSQAMPAVEATLMKSYADVHOUVSADARLMLQOLEEKGRYAKDVMA 1047

DB 625 IYVCGDARNARADVONTFYDVAELGAMERHAQVADYIKLMTKGRYSLDWS 676
 RESULT 9
 NCPR_CAVPO STANDARD; PRT; 677 AA.
 ID NCPR_CAVPO
 AC P37039;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
 GN POR.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley;
 RA MEDLINE=93041995; PubMed=1420354;
 RA Ongiva S., Goda T., Ishizaki K., Kametaki T., Shiraiki N.;
 RT "Molecular cloning and sequence analysis of guinea-pig NADPH-
 cytochrome P-450 oxidoreductase.";
 RL Biochim. Biophys. Acta 1171:103-105(1992).
 RN [2]
 RP ERRATUM.
 RX MEDLINE=9386164; PubMed=8373812;
 RA Ongiva S., Goda T., Ishizaki K., Kametaki T., Shiraiki N.;
 RL Biochim. Biophys. Acta 1174:313-313(1993).
 CC -1 FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 TO CYTOCHROME P450 IN MICROSOES. IT CAN ALSO PROVIDE ELECTRON
 CC -1 CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 ferricytochrome.
 CC -1 COFACTOR: FAD AND FMN.
 CC -1 SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM. ANCHORED TO THE
 ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1 SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 REDUCTASE.
 CC -1 CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM MOUSE.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D10498; BAA01385.1; -.
 DR PIR: S27158; S27158.
 DR HSSP: P00388; IAMO.
 DR InterPro: IPR003097; FAD_binding.
 DR InterPro: IPR001709; FPN_cyt_redctse.
 DR InterPro: IPR001094; Flavodoxin like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00175; NAD_binding_1.
 DR Pfam: PF00258; Flavodoxin; 1.
 DR Pfam: PF00667; FAD_binding; 1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 KM Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KM Membrane; Acetylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT NP_BIND 169 200 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 313 324 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 450 460 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 529 547 NADP (RIBOSE PART) (BY SIMILARITY).


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Db      385 ELAEY--CSDEKDEKFEPRNMAST---PE-----GKEKYQWIONSSRNHIEDI 431
Qy      808 PACMKRSEFIALPSPRRYRYSISSPRVDEKQASTIVSVSEANSGVGEYGLASNY 867
Db      432 KSCPPIDHICELLPRIQPRYSSISSSKLPTNVHTAVVQYETPLGRVN-KGVATSY 490
Qy      868 LAELQE-GDT-ITCFISTPOSEFTLPKPEPTPLIMVPGTGVAPFRGVAQARKOLEOG 924
Db      491 MKENKPSVGEYKVAVFIR--KSCPRLPKSPKIPIMVPGTGLAPFRGFIQERQFLRDGG 548
Qy      925 QSLGEALHYGCRSPHEDYLYQSELENAQSEGITTLTAFSRMNPQPTTYQVHWEDGK 984
Db      549 KVVQDITLYFGCRKDEDFIYRELEQYVQNGTTLTKTAFSR-DQCEKTYVTHLEDDAD 607
Qy      985 KLIELL-DQGNHFYICGDSGMAFAVEATLMKSVADHVSADARLMLQOLEKGRYAK 1043
Db      608 LMKVIGEQKHFIYICGDAKMAVDVKNILVKILSTGKMMNSDAVOYTKMEAKRISA 667
Qy      1044 DVMA 1047
Db      668 DVMS 671

RESULT 11
NCPD DROME STANDARD; PRT; 679 AA.
ID NCPD DROME STANDARD; PRT; 679 AA.
AC 027597; 09VMP2;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P45OR).
GN CYP OR CG11567.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
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RN SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RP STRAIN=Canlon-S; TISSUE=Antenna;
RC MEDLINE=97311413; PubMed=9168130;
RA Hovemann B.T., Sehlmeyer F., Malz J.;
RT "Drosophila melanogaster NADPH-cytochrome P450 oxidoreductase:
RT pronounced expression in antennae may be related to odorant
RT clearance."
RL Gene 189:213-219(1997).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekstra R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Barker E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baas A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshak S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Buttle K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fodor C., Gong F., Gorrell J.H., Gu Z., Guan P., Glasser K.,
RA Glöckner A., Gong F., Gorrell J.H., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoatlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai X.,
RA Laake P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mikhaylov G., Mishina N.V., Mobarry C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusseren D.R., Paclele J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
CC TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON
CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5. MAY FUNCTION TO
CC CLEAR THE OLFACTORY ORGAN (ANTENNAE) FROM ACCUMULATING CHEMICALS.
CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
CC ferricytochrome.
CC -1- COFACTOR: FAD AND FMN.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: HIGH IN ANTENNAE.
CC -1- DEVELOPMENTAL STAGE: EMBRYOS AND ADULTS.
CC -1- SIMILARITY: THE FAD-BINDING DOMAIN IS RELATED TO BACTERIAL
CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
CC REDUCTASE.
CC -----
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CC or send an email to license@sdb-sib.ch).
CC -----
DR EMBL; X93090; CA63639.1; -
DR EMBL; AE003613; AAF52367.1; -
DR HSSP; P16435; 1B1C.
DR FlyBase; FBgn0015623; Cpr.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001709; FPN Cyt. reductase.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR Pfam; PF00175; NAD_binding.1.
DR Pfam; PF00258; Flavodoxin.1.
DR Pfam; PF00667; FAD binding.1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
KW Membrane.
FT NP_BIND 176 207 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 320 331 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 457 467 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 537 555 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 632 648 NADP (ADP PART) (BY SIMILARITY).
FT CONFLICT 38 39 AA -> VT (IN REF. 1).
FT CONFLICT 45 45 S -> T (IN REF. 1).
FT CONFLICT 132 132 I -> T (IN REF. 1).
SQ SEQUENCE 679 AA; 76346 MW; C6387C111A0DB8A CRC64;
Query Match 13.3%; Score 725.5; DB 1; Length 679;
Best Local Similarity 22.8%; Pred. No. 2.4e-33;
Matches 191; Conservative 113; Mismatches 257; Indels 79; Gaps 21;
Qy 460 SPSTEGAKYKRAKKAENAHNTPLLVYGSNMGTAGTARLADIAMS---KGFA--POVA 514
Db 67 SASDNSFTKLUK-----ASGRSLVVFYGSQTGEERAGRLAKGIRYRLKGMVADFEBC 121

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Oy 515 ILDS--HAGNI-PREGAVILVTSYNGHPDPAKQVDMIDQASAEVGVRSYVGCGRK 572
Db 122 DMEBILQJLKDIDNSIAVFCIAFYGGEDPFDNMEFEYEMITTSGDV-LISCLANYAVGLGRK 180
Oy 573 NMATTYOKVPAFIDETLLAKAGAEINADRGEADASDFFEGTYEEMREHMSDVAAPFNLDI 632
Db 181 TY-BHYNNVAVIYVDRKRLBELGANNRFELGLDGDANDIEDFTWMDRFPANCDFHG--I 237
Oy 633 ENSEDNKSTLSIQFVDSAADNF-----LAKCH-----GAFSTNVVASKELQ 673
Db 238 EGGGEVILROYRLLEQDPVQDRITYTGHEIALHSIONRPPFDKAPFLAPIKYNREIH 297
Oy 674 QPGASRSTRHLEIPL-KEASYQEBDHGVI PRNTEGYNNRTARFGIDAS--QOINLE 729
Db 298 K-GGGRSCMHIELSTIEGSRMDYDAGDHVAMFVNKSLVEKJGQJCNADLDTVFSLINTD 356
Oy 730 ABEELKLAHP-----LAKTVSEVLEQVYELQDVPVTRTQJRAAAKTV 772
Db 357 TDSKSKHFPCCYTRYRTALTYHLEITAIPTHILKELAEY--CTBEKEKELLSMA--SI 412
Oy 773 CPHKVELLEALLEKQAYKEQVLAKELTMLELLEKYPACEMKSEFTALPISIRPYYSIS 832
Db 413 SPE-----GKEKYOSWIDQACRNVIHLEDIKSCPPIDHCELLPRLOPRYSIS 463
Oy 833 SSPRVDEKQASITTVSVSGEAMSGYGEYKGIASNTLAEIQ---EGDITCTISIPQSEF 888
Db 464 SSARKHPFDVHTAVLVEKYKPTPTGIN-KGVAITYLLKPKKQPGSGSEEVKVPPIR--KQOF 520
Oy 889 TLPKDPEPTLIMVGGGTGVAPRGRVQVQARKOLEGOSISGEAHLEFGCSPHEDITYOBE 948
Db 521 RLPTKEPEPTIIMVGGGTGLAPFRGITOERQPLRDEGKTYGSEILYFGCRKMSBEDVITYBEE 580
Oy 949 LENAQSEGIITLHTAFSSRMWNPQPTYVOHVMEQDQEKULIELLDQG-AHFYIIGDGSQMAP 1007
Db 581 LEEWYKKTGLNLKAFPSRDQCG-KYVVOGLLEQDADLLIMVNIENKNGHYIICGDACMAV 639
Oy 1008 AVEATLMSYADVHOVSEADARLMLQOLEKERYAKQDWA 1047
Db 640 DVRNITVLKILSTKGMMSBADAVOYIKRKMAQRYASADWVS 679

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RESULT 12	ID	NCPR_SALT	STANDARD;	PRT;	601 AA.
AC	PI9618;				
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R)				
DE	(Fragments).				
OS	Salmo trutta (Brown trout).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.				
OX	NCBI_TaxID=8032;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=88008061; PubMed=3116019;				
RA	Urenjak J., Linder D., Lumper L.;				
RT	"Structural comparison between the trout and mammalian hydrophilic				
RL	domain of NADPH-cytochrome P-450 reductase.";				
RL	J. Chromatogr. A 397:123-136(1987)				
CC	-1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP				
CC	TO CYTOCHROME P450 IN MICROSOMES. IT CAN ALSO PROVIDE ELECTRON				
CC	TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.				
CC	-1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2				
CC	ferricytochrome.				
CC	-1- COFACTOR: FAD AND FMN.				
CC	-1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE				
CC	ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.				
CC	-1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL				
CC	FLAVOPOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN				

CC	NADP; REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE REDUCTASE.
DR	PIR; A28577; A28577.
DR	HSSP; P16435; 1B1C.
DR	InterPro; IPR001709; FPN_cyt_redtase.
DR	InterPro; IPR001094; Flavodoxin_like.
DR	PRINTS; PR00369; FLAVODOXIN.
DR	PRINTS; PR00371; FPNCR.
KW	Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum; Membrane.
FT	NON_TER 1
FT	NON_CONS 426 427
FT	NON_CONS 434 435
SQ	SEQUENCE 601 AA; 68304 MW; BC801767DEID44C9 CRC64;

Query Match	13.2%;	Score 723;	DB 1;	Length 601;
Best Local Similarity	30.2%;	Pred. No. 2.8e-33;		
Matches 195;	Conservative 106;	Mismatches 239;	Indels 106;	Gaps 21;

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0Y 459 P$P$TEGSA--KYVKKAEANAHNTPLLVILG$NMNGT$EGTRADLADLAMS$KGA$PQVATL 516
Db 5 PAB$TQ$T$F$EKKAKKTGRN-----IYF$G$Q$T$GTE$E$F$N$R$K$A$H$R$G$M$S$M$A$D$P 59
0Y 517 D-----SHAGNLPREGAVLIV--TASY-NGH$P$D$N$A$Q$F$D$M$L$D$A$S$A$D$E$V$G$V$Y$F$G$C 569
Db 60 E$Y$M$S$E$L$R$L$A$E$I$G$N$S$I$A$F$C$A$T$Y$G$E$G$D$P$T$N$A$Q$F$D$M$L-Q$E$T$Q$Q$G$S$G$V$N$Y$P$E$A$L 118
0Y 570 G$D$K$M$A$T$T$Y$Q$K$V$P$F$I$D$E$L$T$A$K$A$E$N$I$A$D$R$G$E$D$A$S$D$D$F$E$G$T$Y$E$E$M$R$E$H$M$S$D$V$A$A$Y$N 629
Db 119 G$D$K$Y--E$H$Y$M$A$G$Y$V$V$K$R$L$E$E$L$A$K$A$V$F$D$G$M$D$D$D$G$N$E$D$E$V$T$W$R$E$O$P$M$P$M$C$E$F$G 177
0Y 630 L$D$I$N$S$E$D$N$K$T$S$L$O$F$V$D$S$A$D$P$L$A$K$M$-----G$A$F$S$T$N$V$A$S 669
Db 178 V$E$A$G$E$D$S$S$V$R$Q$Y$E$L$K-----E$H$N$D$I$N$N$K$N$V$T$G$E$L$G$R$L$K$S$F$E$T$Q$K$P$P$D$A$K$P$F$L$A$P$T$V$N 234
0Y 670 K$E$L$O$Q$P$S$A$N$T$R$L$E$I$E$L$P--K$E$A$S$Y$O$E$G$D$H$G$V$I$P$N$V$E$G$I$V$N$R$V$T$A$R$F$G$L$D$A$S$Q$O$I$R$L 728
Db 235 R$K$L$N$K$A$E$L$H$K--M$E$L$E$V$D$I$T$G$S$K$I$R$E$S$G$H$V$A$Y$P$T$N$N$T$V$Y$V$N$R$L$Q$I$G$L$V$D$D$S$V$S$L 293
0Y 729 E$A$E$E$K-----L$M$L$P$L$A$K$T$V$S$E$L$L$O$Y--V$E$L$O$D$P$T$R$Q$R$L 765
Db 294 N$N$D$E$S$N$K$K$H$P$P$C$P$T$T$Y$T$A$L$T$H$Y$D$I$H$P--R$T$N$V$L$E$L$Q$V$A$T$D$L$D$Q$E$N$T$S$M$A 351
0Y 766 A$M$A$K$T$V$C$P$H$K$V$E$L$A$L$E$K$O$A$Y$K$E$O$V$L$A$K$R$L$M$L$E$L$E$K$Y$P$A$C$E$M$K$F$E$F$I$A$L$P$S$I$R 825
Db 352 S$S$A$E-----G$K$A$L$Q$S$V$L$E$D$N$R$N$I$A$L$B$E$L$P$S$L$R$P$D$I$D$L$C$E$L$M$R$L$Q 397
0Y 826 P$R$Y$I$S$S$P$R$V$D$E$K$O$A$S$I$V$S$V$S$G$E$A$M$S$G$E$Y--K$G$I$A$S$N$Y$L$A$E$L$Q$E$D$T$T$C$F$I$S$T 883
Db 398 A$R$Y$S$I$A$S$S$K$V$H$E$N$S$I$H$I$C$A$V$L-----E$Y$T$K$G$V$A$T$M$L$K$I$R-----437
0Y 884 P$O$E$F$T$L$P$K$D$E$P$L$I$W$G$E$T$G$V$A$P$R$G$F$O$A$K$O$L$K$E$G$O$S$I$G$E$M$L$Y$E$G$R$S$P$H$E$D$Y 943
Db 438 -K$O$F$R$L$P$F$K$A$N$D$V$I$W$G$E$T$G$I$A$P$M$G$F$I$Q$E$G$M$L$E$S$K$E$V$E$T$V$L$Y$G$C$H$K$E$D$Y 496
0Y 944 L$Y$O$E$L$E$N$A$O$E$G$I$T--L$H$T$A$F$S$M$P$O$K$T$Y$V$O$W$H$E$O$D$E$K$U--I$E$L$D$G$A$F$I$Y$C$D 1001
Db 497 L$Y$O$E$L$O$A$H$K$K$G$A$L$T$K$L$N$A$F$S$R$E$D$O--K$Y$V$O$H$L$R$K$K$V$D$M$R$Q$I$H$E$D$Y$A$H$I$Y$C$D 555
0Y 1002 G$S$O$M$A$P$A$V$E$A$L$M$S$Y$A$D$V$H$O$V$S$A$D$A$R$L$M$L$O$U$E$E$G$R$A$K$U$Y$A 1047
Db 556 A$R$N$A$R$D$V$O$T$A$F$Y$E$I$A$E$L$G$M$T$O$A$T$D$Y$I$K$L$M$I$T$G$R$S$O$D$W$S 601

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RESULT 13			
NCPR PHAU			
ID	NCPR PHAU	STANDARD;	PRT; 690 AA.
AC	p37116;		
D1	01-OCT-1994	(Rel. 30.	Created)
D1	01-OCT-1994	(Rel. 30.	Last sequence update)
D7	16-OCT-2001	(Rel. 40.	Last annotation update)
DE	NADPH-cytochrome P450 reductase	(EC 1.6.2.4)	(CPR)
D5	Phaseolus aureus (Mung bean)	(Vigna radiata)	(P450R)

CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
 CC NCBI_TaxId=3916;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC STRAIN=cv. Beiken; TISSUE=seedling;
 RX MEDLINE=93219390; PubMed=8464904;
 RA Sheet M.S., Sathasivan K., Arlotto M.A., Mehdy M.C., Sababrook R.W.;
 RT "Purification, characterization, and cDNA cloning of an NADPH-
 RT cytochrome P450 reductase from mung bean."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2890-2894 (1993).
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferriocytocrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- PTM: GLYCOSYLATED.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN
 CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 CC -----
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 CC or send an email to license@sib-sb.ch).
 CC -----
 DR EMBL: L07843; AAA34240.1; --
 DR HSSP: P00388; 1AM0.
 DR InterPro: IPR003097; FAD binding.
 DR InterPro: IPR001709; FPN_cyt_reductase.
 DR InterPro: IPR001094; Flavodoxin-like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR001433; Oxred FAD/NAD(P).
 DR Pfam: PF00175; NAD binding_1.
 DR Pfam: PF00258; flavodoxin; 1.
 DR Pfam: PF00667; FAD binding_1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 KW Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane; Glycoprotein.
 FT NP_BIND 179 210 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 325 336 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 465 475 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 544 562 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 639 654 NADP (ADP PART) (BY SIMILARITY).
 FT CARBOHYD 275 275 N-LINKED (GLUCANIC...) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLUCANIC...) (POTENTIAL).
 SQ SEQUENCE 690 AA; 76506 MW; 592966167E8561DE C6C64;
 Query Match 13.2%; Score 721; DB 1; Length 690;
 Best Local Similarity 30.6%; Pred. No. 4.4e-33;
 Matches 191; Conservative 109; Mismatches 259; Indels 66; Gaps 19;
 QY 477 AHNTPLLVYSGNNGTAGTARLAD--IAMSKEFAPVATLDSHAGN-----LPRFG 527
 DB 77 AGKTKVITFGTGTAGFAKALAEIKARYEKAAYVLDVADDDVEEELKKES 136
 QY 528 AVLVTASY-NGHPRDAKQFMDLQASADE---VKVRSVRECCGKMATTYQKPA 583
 DB 137 LVFPMLATVYGGEPLDNARYFKYFTEKDRGWLQKLTGYVFLGRQY-EHNNKIGK 195
 QY 584 FIDETIAKGAENIADGEADASDDFEGTVEEYRHHMSDVAAYNLDIENSDDKSTLS 643
 DB 196 VDEELAEAGAKRLVAVAGLGGDDDSIEDDFSMKESLSELD-----QLADEDDANIVS 250
 QY 644 LQFVDSAADM-----PLA-----KMGAFSTNVVASKELQPGSARS 680

DB 251 TPPTAALLEVRVINDPTASTYDNNSTVANGNTFEDIHPCVAVAVQELKPSDSKS 310
 QY 681 TRHLEIELP-KEASYOGDHLGVI PRNYEGIVNRVTFARFGLDASQOIRLEAEKLAHL- 738
 DB 311 CHLEPDIQSTSTITDTGHDVGYAENCNFETVETKLGQNDLDFSLHTDMDGSLG 370
 QY 739 -----PLAKTVSE-ELQYVELQDPVTRTQLPAMAKTVCPPHKVELEALL- --KQAY 789
 DB 371 GSLPFPFGCSRTALARYADLLNPRKALLALATH-ASEPSDEKTELSSPOGDEXY 429
 QY 790 KEQVLAKRLMLLEKVPACENKFESEFI-ALLPSIRPRYSISSSPRVDEKASITVSV 848
 DB 430 SKWVVSQRSLVEMVMEFPSPAKPPLGVFPALAPRLOPRYSISSSPRPAPQVHTCAL 489
 QY 849 VSGEAMSGVEYKIGISNYL-----AELOEGDTTCFISTPOSEFTLPDPETPLIMWG 902
 DB 490 VYGPETFG-RIHNGVSTWMMKNAIPSKSDCSAPFIR--PSNPLPVDHSIPLIMWG 546
 QY 903 PGTGVAFRGFGVQARKQKEQSGSLGEALVFCGRSPHEDVLYOELENAQSEGIIT-LH 961
 DB 547 PGTGLAFPRGFLQBRVALKEDGVQLGPALEFPCGRNQMPFIVEDELKSFVEQSGISELI 606
 QY 962 TARSMPNQKTYVQVHMEQDGKLLIEDQGAHFYICGEGSQMAPVAVEATLTKSVADVH 1021
 DB 607 VAFSR-EGAEKEYVQHKMDKAHLWSLISQGYLYVCGDQAKMARDVHRTLHSIVQEOE 665
 QY 1022 QVSEADARLWLOOLEEKGRYAKDVM 1046
 DB 666 NVDSKRAEALVYKLGMDGRRLRDVM 690

RESULT 14
 NCPR CATRO STANDARD; PRT; 714 AA.
 AC 005001;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (P450R).
 GN CPR.
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
 CC Vinceae; Catharanthus.
 CC NCBI_TaxId=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94035173; PubMed=8220474;
 RA Meljor A.H., Lopes Cardoso M.I., Voskuilen J.T., de Waal A.,
 RA Verpoorte R., Hoge J.H.C.;
 RT "Isolation and characterization of a cDNA clone from Catharanthus
 RT roseus encoding NADPH-cytochrome P-450 reductase, an enzyme essential
 RT for reactions catalysed by cytochrome P-450 mono-oxygenases in
 RT plants."
 RL Plant J. 4:47-60 (1993).
 RN [2]
 RP SEQUENCE OF 1-11 FROM N.A.
 RC STRAIN=cv. Morning mist;
 RA Lopes Cardoso M.T., Meljor A.H., Rueb S., Queiroz Machado J.,
 RA Memelink J., Hoge J.H.C.;
 RA submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THIS ENZYME IS REQUIRED FOR ELECTRON TRANSFER FROM NADP
 CC TO CYTOCHROME P450 IN MICROSOSES. IT CAN ALSO PROVIDE ELECTRON
 CC TRANSFER TO HEME OXYGENASE AND CYTOCHROME B5.
 CC -1- CATALYTIC ACTIVITY: NADPH + 2 ferricytochrome = NADP(+) + 2
 CC ferriocytocrome.
 CC -1- COFACTOR: FAD AND FMN.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM, ANCHORED TO THE
 CC ER MEMBRANE BY ITS N-TERMINAL HYDROPHOBIC REGION.
 CC -1- SIMILARITY: THE FMN-BINDING DOMAIN IS RELATED TO BACTERIAL
 CC FLAVODOXINS. THE FAD DOMAIN APPEARS HOMOLOGOUS WITH FERREDOXIN

CC NADP+ REDUCTASE, NADH CYTOCHROME B5 REDUCTASE, AND GLUTATHIONE
 CC REDUCTASE.
 CC -----
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 CC -----
 DR EMBL: X69791; CAA49446.1; -;
 DR EMBL: Y09417; CAA70571.1; -;
 DR PIR: S31502; S31502.
 DR HSSP: P00388; JAMO.
 DR InterPro: IPR003097; PAD binding.
 DR InterPro: IPR001709; FPN_Cyt_redctse.
 DR InterPro: IPR001094; Flavodoxin_like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00175; NAD_binding_1.
 DR Pfam: PF00258; Flavodoxin_1.
 DR Pfam: PF00667; PAD_binding_1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 DR Oxidoreductase; Flavoprotein; FMN; FAD; NADP; Endoplasmic reticulum;
 KW Membrane.
 FT NP_BIND 200 231 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 348 359 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 489 499 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 567 585 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 661 677 NADP (ADP PART) (BY SIMILARITY).
 SQ SEQUENCE 714 AA; 78958 MW; DBDD9AF41374CF91 CRC64;
 Query Match 12.9%; Score 702; DB 1; Length 714;
 Best Local Similarity 28.8%; Pred. No. 5,4e-32;
 Matches 189; Conservative 118; Mismatches 274; Indels 76; Gaps 18;
 QY 445 VNAKSKKIPLGIPSPTEQSAKVKKAKNNHTPLVLVYSGNMGTAEGTARDLADIA 504
 DB 79 VVEPKLIIVKSVVEPEIDEGKK-----FTTFPGTGTAGPFAKALAE 126
 QY 505 MSK-GRAPQVATLDASHN-----LPREGAVLIVTASY-NGHPDNKQFVMDLQA 554
 DB 127 KARYEKAVIKVIDIDVAADDEYEKFKETLAFFILATYGOEPTDNARFYKPFVEG 186
 QY 555 S--ADEYKGRYVFGGDKGMATYKQVAFIDETLAAGAERIADRGADSDPEGT 612
 DB 187 NDRGDMVKMLQYGVFGIGNQY-EHFNKIAKVDEKVAEOGKRIYELVIGDDOCIEDD 245
 QY 613 YEERHEHMGSDVAAYFNLDIENSEDNKSTLQFV-----DSAADMLAKMHGAF 662
 DB 246 FAAMRENVWR-----LDNLARDEDDTVTYTAIPEYRVVFPKPSLSISEANGHA 299
 QY 663 S-----TNVASKELQOQPSASTRLIELEPKEA-SYQEGHILGVIPR 705
 DB 300 NGYANGTVYDAQHPGRSNVAVRKELHTPASDRSCTHLDPIAGTSGYGGHVGYYCD 359
 QY 706 NYGGINVRYARFGDASQOIRLEAEKEKAHL-----PLAKTVSVEELLQYVELQDP 758
 DB 360 NLSETEVEARLNLNLPETVPSLHADKEDGTPLAGSSLPFPFPCCTLRATLRVADLNT 419
 QY 759 VTRTQLRAMAAKTVCPPHKVELLEALL----KQAYKEQVLAKRJLMLLEKYVAPCEMKFS 815
 DB 420 PKRSALLALAAVYSDPEADRLKTLASPAKDEYAGSLVANOSLSLEFVMAEPFSAKPLG 479
 QY 816 EFL-ALLPSIRPVYSSISSPRVDEKQASITVSVSEAMSGYGEYKGIASNYLA----L 871
 DB 480 VFPAALAPRLOPRFYSSISSPRMAPSRIVHTCALVY-EKTPGGRIRHGVCSTMMKAIPL 538
 QY 872 QEG-DITTCISTISPOSFTLPKDPETPLINVGRETGVAPRGVQARQKOLEGOSIGEA 930
 DB 539 EESRDGSGWADI FVQGSNFKLPADPKVYVIMIGPOTGLAPFRGFLQERLALKEGAEIGTA 598

QY 931 HLYFGCRSPHEIDYLYOEBLEMAQSEGIIT-LHTAFSRMPNPQRTYVQHWEDQKKLIEL 989
 DB 599 VFPPGCRNRMKMDIYDELDINHFLIEGALSELVAFSR-EGPTQYVQHKAEXASDIWM 657
 QY 990 LDOGAFYICGDSQMAPAVEATLMKSYADYHOVSADARLMIQOLEKRYAKDW 1046
 DB 658 ISDGAVVYCGDAKGMARVHRTLHTIAOEGSMDSIOEGFVKNLQMTGRYLRDVW 714
 RESULT 15
 NOS2_RAT
 ID NOS2_RAT STANDARD; PRT; 1147 AA.
 AC Q06518; P97774; Q35765; Q35766; Q64558; Q64005; Q63267;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 GN (Inducible NOS) (INOS).
 OS NOS2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vascular smooth muscle;
 RX MEDLINE=93191721; PubMed=7680561;
 RA Nunokawa Y., Ishida N., Tanaka S.;
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
 RT muscle cells.";
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mistral; TISSUE=Pancreatic islets;
 RX MEDLINE=95309542; PubMed=7540573;
 RA Karlén A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
 RA Charetero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
 RA Mandrup-Poulsen T., Boel E., Nerup J.;
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase
 RT cDNA from rat islets of Langerhans.";
 RL Diabetes 44:753-758(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Astrocytes;
 RX MEDLINE=94231594; PubMed=7513765;
 RA Galea E., Reis D.D., Feinstein D.L.;
 RT "Cloning and expression of inducible nitric oxide synthase from rat
 RT astrocytes.";
 RL J. Neurosci. Res. 37:406-414(1994).
 RN [4]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94039059; PubMed=7693462;
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,
 RA Kawasaki H., Sugimura T., Sumi H.;
 RT "Molecular cloning of a cDNA encoding an inducible
 RT calmodulin-dependent nitric-oxide synthase from rat liver and its
 RT expression in COS 1 cells.";
 RL Eur. J. Biochem. 217:37-43(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Hepatocytes;
 RX MEDLINE=93221515; PubMed=7682072;
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
 RT "Hepatocytes and macrophages express an identical cytokine inducible
 RT nitric oxide synthase gene.";
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta;
 RX MEDLINE=9435351; PubMed=7519448;
 RA Geng Y.J., Almqvist M., Hansson G.K.;

Db 538 VLFATETGKSEALARDIAL-PSYAFNTKVCMEQYKANTLBEBOILLVVTSTFGNDCP 596
QY 542 DNAKQFVMDLDOASADEVKGV---RYSVFGCGDKMWTYYQKVPF---IDETLAKGA 594
Db 597 SNGQTL-----KSLFWMKELGHTFRYAVFGLG---SSWYPOCFAPAHIDQKLSHLGA 647
QY 595 ENIADGGEADSDDEFTGEYEMREHMSDVAAIFNLDIENS-----ED 637
Db 648 SOLAPGEGDELGGQEDAFRSMVQTFR--ACETFPVRSKHCIQIPKRYTSNATWEPBQ 705
QY 638 NKSTLSLOFVDSADMDPLAKQH--GAFSTNVVASKELQOPGSARSTR--HLEIELPKKAS 693
Db 706 YKLTQSPESID--LNKALSSIHAKNVFTMRUKSLQNLQSEKSKRTLLVQLTFEGSKRPS 763
QY 694 YQEGDLGVLPRIYEGIVNEVTAFFGLDAS---QOIRLEAESE-----KLHLPLAKTV 744
Db 764 YLPGEHLGIFPGNOTALVQGLIERV--VDCSSPDQTVCLVLEDESGSYWVKDKRLP---PC 819
QY 745 SVEELLQY-VELODPVRTQLRAMAATVCPPHKVELBALLEKOAYKEQVLAKRLTMLEL 803
Db 820 SLRQALTYFLDITTPPTQLHKLARFATEETHRQRLLEALCQPSBYNDMKFSNNPTFLEV 879
QY 804 LEKYPACEMKFSEFIALPISIRPRYVSISSPRYDEKQASITVSVSGEAMSGYE-YKG 862
Db 880 LEEFPISLRVPAAFILSQLPTLKPRYVSISSQDHTPSEVHLTVAVVYTRTRDGGGPLHGG 939
QY 863 IASNYLAELQEGDTITCFISTPOSEFTLPKDPETPLIMVPGTGVAPFRGVQAR--KQLK 921
Db 940 VCSWTWINLKPEDPVPFCFVRS-VSGFQLPEDPSPCILIGPGTGIAPFRSFWQRLHDSQ 998
QY 922 EOGQSUGEAHLVPGCRSPHEDVLYQEELENAQSEGIITLHTAFSRMPNQKTYVQHME 980
Db 999 HRGILKGGRMVTLVFGCRHPEBDHLQOEMQOEMVRKGVLFQVHTGYSRLPKKXVVDILQ 1058
QY 981 QD-GKKLIEL--DOGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLQOLEE 1037
Db 1059 KEIADVEFSVYHGSQG-HLYVCGD-VKARDVATTLLKLVAAKLNLESEQVEDYFFOLKS 1116
QY 1038 KGRYAKDWM 1046
Db 1117 QKRYHEDIF 1125

Search completed: May 29, 2003, 10:04:36
Job time : 28 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 10:00:23 ; Search time 99 Seconds
(without alignments)
2181.186 Million cell updates/sec

Title: US-10-031-241-35

Perfect score: 5457

Sequence: 1 TTKEMPQPTFGELKNLPL.....RLWLQQLLEKGRYAKDWAG 1048

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTEMBL_21.*
2: sp_archaea.*
3: sp_bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phage.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*
16: sp_virus.*
17: sp_bacteriap.*
18: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1736.5	31.8	1066	3	Q9Y8G7 fusarium ox
2	1462.5	26.8	1115	3	Q9HGE0 Q9HGE0 gibberella
3	961	17.6	527	16	Q9RD76 Q9RD76 streptomyc
4	773.5	14.2	667	11	Q60451 Q60451 cricetus
5	745	13.7	719	10	Q40916 Q40916 pseudocuga
6	739.5	13.6	692	10	Q9SB48 Q9SB48 arabidopsis
7	737.5	13.5	681	10	Q48937 Q48937 petroselinu
8	734.5	13.5	703	10	Q8VX49 Q8VX49 triticum ae
9	717	13.1	712	10	Q9A006 Q9A006 populus bal
10	714.5	13.1	692	10	Q39035 Q39035 arabidopsis
11	711.5	13.0	683	10	Q24424 Q24424 papaver som
12	711.5	13.0	692	10	Q9A008 Q9A008 populus bal
13	711	13.0	692	10	Q43235 Q43235 vicia sativ
14	710	13.0	656	10	Q9FTM7 Q9FTM7 triticum ae
15	709	13.0	711	10	Q9SUM3 Q9SUM3 arabidopsis
16	706	12.9	705	10	Q24425 Q24425 eschscholzi

17	705.5	12.9	588	10	Q96561 Q96561 helianthus
18	705	12.9	639	10	Q48938 Q48938 petroselinu
19	702.5	12.9	712	10	Q39036 Q39036 arabidopsis
20	695.5	12.7	704	10	Q04434 Q04434 pisum sativ
21	694	12.7	321	2	Q9ZHK0 Q9ZHK0 rhodococcus
22	691	12.7	712	10	Q9A007 Q9A007 populus bal
23	690.5	12.7	687	5	Q9NKK3 Q9NKK3 bombyx mori
24	689.5	12.6	1147	11	Q9RW4 Q9RW4 ratius norv
25	684.5	12.5	662	5	Q09590 Q09590 caenorhabdi
26	681.5	12.5	1311	6	Q9BDH6 Q9BDH6 equus cabal
27	680	12.5	701	5	P91555 P91555 diosiphila
28	680	12.5	736	3	Q9HDC2 Q9HDC2 phanerocha
29	669.5	12.3	1147	11	Q9QW28 Q9QW28 ratius sp.
30	668	12.2	630	3	Q9HG14 Q9HG14 phanerocha
31	667.5	12.2	671	3	Q9HFV3 Q9HFV3 rhizopus st
32	665.5	12.2	1145	11	Q8R410 Q8R410 mus musculu
33	661	12.1	1114	4	Q94994 Q94994 homo sapien
34	658.5	12.1	1154	6	Q97604 Q97604 canis famill
35	657.5	12.0	633	3	Q00141 Q00141 aspergillus
36	651.5	11.9	759	3	Q9C498 Q9C498 rhodocorula
37	650.5	11.9	945	6	Q9N175 Q9N175 ovis aries
38	644.5	11.8	730	3	Q8X1W0 Q8X1W0 coriolus ve
39	636.5	11.7	607	16	Q9KF76 Q9KF76 bacillus ha
40	628.5	11.5	605	16	Q32214 Q32214 bacillus su
41	627.5	11.5	506	10	Q96560 Q96560 hellianthus
42	617.5	11.3	710	3	Q9PAE2 Q9PAE2 cunninham
43	615.5	11.3	1055	5	Q968Y4 Q968Y4 physarum po
44	605.5	11.1	1206	11	Q9WTX6 Q9WTX6 cavia porce
45	597.5	10.9	1205	6	Q9TX8 Q9TX8 canis famill

ALIGNMENTS

RESULT 1

Q9Y8G7 PRELIMINARY; PRT; 1066 AA.

AC Q9Y8G7;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)
DE Bifunctional P-450:NADPH-P450 reductase protein (Fatty acid omega-hydroxylase) (P450foxy) [Includes: cytochrome P450 505 (EC 1.14.14.1); NADPH-cytochrome P450 reductase (EC 1.6.2.4)].
DE CYP505.
GN CYP505.
OS Fusarium oxysporum
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5507;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=MT-811;
RX MEDLINE=20564350; PubMed=10995755;
RA Kitazume T., Takaya N., Nakayama N., Shoun H.;
RT "Fusarium oxysporum fatty-acid subterminal hydroxylase (CYP505) is a membrane-bound eukaryotic counterpart of Bacillus megaterium cytochrome P450BM3.";
RT J. Biol. Chem. 275:39734-39740(2000).
RL [2]
RN FUNCTION, AND SUBCELLULAR LOCATION.
RP STRAIN=MT-811;
RC MEDLINE=96271003; PubMed=8830036;
RA Nakayama N., Takemae A., Shoun H.;
RT "Cytochrome P450foxy, a catalytically self-sufficient fatty acid hydroxylase of the fungus Fusarium oxysporum.";
RT J. Biochem. 119:435-440(1996).
RL
CC -I- ACTIVITY TOWARD FATTY ACIDS AS A FATTY ACID MONOOXYGENASE. SHOWS HIGHEST ACTIVITY TOWARD FATTY ACIDS WITH A CHAIN LENGTH OF 12-14 CARBONS. THE REDUCTASE DOMAIN IS REQUIRED FOR ELECTRON TRANSFER FROM NADP TO CYTOCHROME P450.
CC -I- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH + OXIDIZED FLAVOPROTEIN + H(2)O;
CC -I- CATALYTIC ACTIVITY: NADPH + 2 FERRICYTOCHROME = NADP(+) + 2

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CC -1- FERROCYTOCHROME.
CC -1- COFACTOR: BINDS ONE MOLE EACH OF FAD AND FMN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CYTOCHROME
CC P450 FAMILY.
DR EMBL: AB030037; BAA82526.1; -.
DR HSPSP; P14779; IBY.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin-like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR Heme; Monooxygenase; Oxidoreductase; Membrane; Electron transport;
KM Multifunctional enzyme; FMN; FAD; Flavoprotein; NADP.
FT DOMAIN 1 480 CYTOCHROME_P450 REDUCTASE.
FT BINDING 481 1066 NADPH-P-450 REDUCTASE.
FT BINDING 407 407 HEME (BY SIMILARITY).
SQ SEQUENCE 1066 AA; 117925 MW; 6B812369C223DBA CRC64;

Query March 31.8%; Score 1736.5; DB 3; Length 1066;
Best Local Similarity 36.8%; Pred. No. 2.5e-100;
Matches 393; Conservative 190; Mismatches 444; Indels 43; Gaps 19;

QY 5 MPOKTEGELNLPDLNTDKFVQALMKIADLGEIFKEAPGRVTRYSQRLKEACDE 64
DB 7 IPEBPYPLIGNLGEF-TSNPLSDLNRLADTYGPIFLRLGAKXPIFVSSSLINEVCE 65
QY 65 SRPKNLSQALKFRDPAFGDGLFTSWTEKWKAKAHNILLPSECOAMKGTAAWVDIAV 124
DB 66 KRFFKTKSVLSQVREGVHDLPTAFEDBPWGAHRLIVAFPLSLRGVFPFEMHDIAT 125
QY 125 QLVOKWERLNDDEHIEVEDWTRLTLDITGCGFNVRNSFYRQPHFPIFMSVRALDEA 184
DB 126 QLCMKFARHGRTIDISDNTRLALDITLALCANDFRYSYKSELHPIFAMGDFLTES 185
QY 185 MNKLQANPDDP--AYDENKRFQEDIKMNLDLVKTIADRKASGEOSDILLTHMLNGKD 242
DB 186 GNR-NRRPFAFNFLYRAANEKFGDIALMKSVADDEVAAAKKAPSDDKDLAAMLVGD 244
QY 243 PETGEPLDENIRQITITELIAGHETTSGLSPALYFLVKRPHYLQKAAEAAKLVDPV 302
DB 245 POTGEKLSDENITQITITFLIAGHETTSGLSPFMYQLKNPEAYSKVQKEVDEVGRGP 304
QY 303 PSYQVQVKLVGVNLBRLMPTAPFSLYAKEDPTLVGGEVPLEKGDMLAVLIPOLHR 362
DB 305 VLVEHLTKLPITSAVLRETLRLNSPTIRFGLEALIDDTFLGSKVLVKGSEIYATLISRHV 364
QY 363 DKTIWGDVEERPER-----FENPSAIPQAFKPFNGGQACIQOQFALHEATLVLMGM 417
DB 365 DPVVGADNADKFIERMLDDEFARLNKEYPWCWKPFGGKACIGRPAPWGESLAAVVL 424
QY 418 LKHPDFE-DHTNYELDIKETLTLPKREGVVAKSKK-----IPLGIPSPSTEOS 466
DB 425 FQNFNFTMTDNPVLALEIKQITLTKPDHFYINATLRHGWTPELEHVLNAGNATSSSTINI 484
QY 467 AKYRKKAENAHNPLVLVGSNMGTAGTARLADLAMSGF-APQVATIDSHAGNLR 525
DB 485 KAAINLDKAGSGKPMALFYSGNSGTALANRLASDPSSHGFATYVGPIDQAKQNP 544
QY 526 EGAVLITASYNGHPDPAKQFVDMLDQASADEVGVVYVFGCGDKMATTYOKVPAFI 585
DB 545 DRPVVITASYEGQPSMAHFIKMBDLDDGDMKESYAFACGHHDWVTFHRIPLCV 604
QY 586 DETLAAGAENIADRGAD-ASDDEFTGEYEWRE-HMMSDVAAVFNLDIENSEDNKSTLS 643

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DB 605 DSTLEKGGTRILPMGADAAATSDMPSDFEAMBDIVLMPGLKERYKTSDESGGQKLL- 663
QY 644 LQFVDSADWPLAKMHGAFSTNNVASKELOQPSASSTRLEIELPEASVQEGDHLGVI 703
DB 664 ---VEVSTPKRTSLRQVEBALVAEKTILKSGPAK--KHIELQPSAMTYKAGDYATIL 718
QY 704 PRNVEGIUNVTARFGIDASQOIRLEAEERKLAHLPLAKTVSVEELIQ-YVELDPVTRT 762
DB 719 PLNPKSTVARVFRFSPILAMSPFLKIOSECP--TTLPTNVASISAFVDSAYVELSQPATKR 776
QY 763 QLAMAKTYCPRHUKLELLEKQAYKEQVLAKRULMTELLEKYPCEKPFSEFIALP 822
DB 777 NILALAEATDKDTIOELER-LAGDAQATISPRVSVLPLEKFPVALPISYLMLP 835
QY 823 SIRPRVYSSSPRVDEKQASITVSVSGEAMSGYGEYKSIASNYLAELQEGPTTCFIS 882
DB 836 PMRVQYSSISSPPADSKTLTYSLDASLSGGQGHVAVNPLSHLTAGDKLHVSVR 895
QY 883 TPQSEFTLPKDPF-TPLIMVPGTGVAFFRGVQARKQLEQCSQSGEAHLFYGCSPHE 941
DB 896 ASSAPFLPDADKPTPIICVAGTGLAPLPGFIOERAAMLAARLTLPALLFGCRNPEI 955
QY 942 DLYQELLENAGSEGITTLTAFSRMPNOK--TYQVHNEQDQKLEILLDQAHNYIC 999
DB 956 DDLVAEEFERMEKXGAVDVARAVSRATDKSGCKYVQDVRVHRAVDFKWDGAKVFC 1015
QY 1000 GDGQMAVPE-----ATLMKSYADVHQVSEADARLMLQLEEKGRYAKDW 1046
DB 1016 G-SREIKAVEDVCVRAIEKAOQNGRDVTEWARRAMFERSRNE-RATIVP 1065

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RESULT 2
Q9HGE0 PRELIMINARY; PRT; 1115 AA.
AC Q9HGE0;
ID Q9HGE0;
DT 01-MAR-2001 (Tremblrel_16, Created)
DT 01-MAR-2001 (Tremblrel_16, Last sequence update)
DT 01-JUN-2002 (Tremblrel_21, Last annotation update)
DE FumGp.
GN FUMG.
OS Gibberella moniliformis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocitaceae; Nectriaceae; Gibberella.
OX NCBI_Taxid=117187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M-3125;
RA Proctor R.H.; Seo J.-A.; Plattner R.D.;
RT "Characterization of four clustered and coregulated genes associated
RT with fumonisin biosynthesis in Fusarium verticillioides.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL: AF155773; AAG27132.1; -.
DR HSPSP; P00386; 1092.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003097; FAD_binding.
DR InterPro: IPR001094; Flavodoxin-like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR001709; FPN_cyt_redctse.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00667; FAD_binding; 1.
DR Pfam: PF00258; Flavodoxin; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 1115 AA; 123276 MW; 5C6D2B947AE86C25 CRC64;

Query Match 26.8%; Score 1462.5; DB 3; Length 1115;

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Best Local Similarity 33.7%; Pred. No. 4.5e-83;
Matches 380; Conservative 195; Mismatches 439; Indels 113; Gaps 32;

QY 2 IKEMPOKTEGELKLNPLNTDKPVQALMKIADBLGIFKEAP-----GRYTRYV-SS 54
DB 19 LRPIPKPKPLPLGNLFDPPD-----NLTKSLGSLGKHPIYITGASTEMWTS 71

QY 55 QRLIKACDSRSPDKNLSQLKVRDPADGDLFTSWTHKXKXKXNILLPSFSQAMKG 114
DB 72 REIAQELCDRETRCKLPGALDWKAVGDGLFTAETSNPKMAIARIITPLFGAMIRG 131

QY 115 YHAMMDIANVQVKMERLNADENIEIPEDMTRLTDTGLCGENYFNFSYRDQ--PH 172
DB 132 MFDMDKDICQMKLRMARFEPDEPLNCDMTKLTDTLTALCTIDYFNFSYRNGAHP 191

QY 173 FITSMVALDEANMKLORAND-----DPAYDENKQFOEDIKVNDLVDKIADKA 225
DB 192 FALAAYDVMTESD--QSNLPDFVNNYVRRAAKFKRQAAE---LRQTEBILARRQ 245

QY 226 SGEOSDILLTMLNGKDPETGEPLDENIRYQITPLIAGHETTSGLSPALYLVNPH 285
DB 246 NPVDRDLNAMLASAKDKPTGEGSPESIVDNLITFLIAGHETTSLSLSCFYLLNPH 305

QY 286 VLOKAAEAAVLDVPVSYKQVKQKLYGVNLTNEALRLMPTAPASLYAKEDTVLGEY 345
DB 306 VLRVQOEVDTVVGSDDITVDHLSMPEYLRVLRRLRDPGPFYVKKLDEVVAGKY 365

QY 346 PLKGBELMWLILQIHRDKTIWGDVDEPRPERF--ENSAIPQHAARPGNGORACIQ 403
DB 366 AVNKQDPLFIVPVSVDQSTYGDADDEFERPERLKGKGPDKLPCAKARKPGNGRACVGR 425

QY 404 QPALHEATVLGMLKHFDEEDHTNVELDKETLLTKRSGFVVAKSK-----IPLGG 457
DB 426 PFMQQAIIAIVANVILKFDLVKDESYTLKXHVMTVA RVGTIMKVRRLRQGRATDLAMGL 485

QY 458 IBSPTSTQSKAKYKKA-----ENANTPLVITYGSMGTAEGLADLADIAM 505
DB 486 HRHSGEASAPSPRASLRKLSDVNGDDTDHKSQIAVIVASNSGCEALAVRLAEAT 545

QY 506 SKGFAPVATLDSHA--GNLPREGAVLITVASYNHGPDMNKOPFMDLQDQASADVEKVRY 564
DB 546 ERGFGIRAVDVNNALIDRIVGSGVILITVSYNGEPADDOEFVPMKLSLSEGLNKKVF 605

QY 565 SVFGCGDKMATTYQKVPAFIDETLAKAGANIADRGESADSP-----DFEGTYEEMRE 618
DB 606 AVFNGHRDAMANTLPANPRILIDSELACGAEVRSIMGVSTCCSSDPSFSE----- 657

QY 619 HMMSDVAAYFNLD-----IENSNDKSTLSIQFVDSAADMLAKHGAFTNVVA--SK 670
DB 658 -RWIDEKLPPELETPHGGGVKNGDRAVPRQELQV--SLGQPRITWRKGVYRAIVTEAR 714

QY 671 ELQOPGSARSTRLEIELEKESAYQEGDHGVI PRNVEGIVNRTAFEGDASQIRLEA 730
DB 715 SLSSPG--VPEKRHELELPDFONFKADHDHYILPRNSPRDVVALSYFGEDTLITRN 773

QY 731 EEEKLA--HLPLAKTVSEELL--QVELQDVTET--QURAMAAKTVCPH--KYELLEALL 785
DB 774 TARKSLGRLDLPITITDGLAVEL-----GRASLKNMTLVDAHGSRRALLSLTE 829

QY 786 KQAYKEOVNLAKLMTLELKYKPAKEMKFEFIALLPISPRYSSISSPRVDEKQASIT 845
DB 830 PERFRAEVDORHYSIIDLLERFPIDISTLSCFLPMLAQIPRAVSFSSADPMKRGHATLT 889

QY 846 VSVV-----SGRANS---CYG---EYKGIANSYLAELQEGTITCISTPSEF 888
DB 890 YTVAVDPTPATQINGSSSKKAVGDDTAIVVORQGLASSYSSGPGSLVYSLHRASPYF 949

QY 889 TLKPDPTPLIMVPGTGVAPFGFVQARKOLKEQG--QSLGEALILYGRSPHEDYLYOE 947
DB 950 CLQKSTSLPIVMGAGGLAFRAFLQERMAABGAQORGPALLFFCGCGPRLDLSYSV 1009

QY 948 ELENAOSEGIITLHTAFSRMPN--OPKTYVOHVEQDK---KILELIDQAHFYICDGS 1003

DB 1010 ELEAYTIGLVQVRAYSDDPSA4QAGCKYTTDRJLCKRDEVARILMDGAQVLYCG--GK 1068

QY 1004 QNAPAVEATIMKSYADVHOV--SEADARL---WLOQLEEKGRYAKDYW 1046
DB 1069 KMANDLVAVGPMLEIDQKRGTTAKTVEMEARL--DKSRVYEEVY 1114

RESULT 3

ID Q9RD76 PRELIMINARY; PRT; 527 AA.

AC Q9RD76;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Putative cytochrome P450.

GN SC00801 OR SCF43.12.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RL Saunders D.C., Harris D.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RL Thomson N.R., Parkhill J., Barrett B.G., Rajandream M.A.;

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RC MEDLINE=97000351; Pubmed=8843436;

RA Redenbach M., Kleiser H.M., Denepaite D., Eichner A., Cullum J.,

RA Kinaishi H., Hopwood D.A.;

RT "A set of ordered contigs and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsey T., Howarth S.,

RA Huang C.H., Kleiser J., Larke L., Murphy U., Oliver K., O'Neill S.,

RA Rabbittowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DR EMBL: AL136502; CAB66201.1; -.

DR HSSP: P14779; 1BYV.

DR InterPro: IPR001128; Cytochrome_P450.

DR InterPro: IPR000217; Tubulin.

DR Pfam: PF00067; P450; 1.

DR PRINTS: PR00385; P450.

DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.

DR PROSITE: PS00227; TUBULIN; 1.

KW Heme; Monooxygenase; Oxidoreductase.

SQ SEQUENCE 527 AA; 57741 MW; 4A612C1B7A894780 CRC64;

Query Match 17.6%; Score 961; DB 16; Length 527;
Best Local Similarity 41.9%; Pred. No. 4.3e-52;
Matches 211; Conservative 80; Mismatches 177; Indels 36; Gaps 10;

QY 2 IKEMPOKTEGELKLNPL-----NTDKPVQALMKIADBLGIFKEAPGRVTRYLSQ 55
DB 27 LHRIPHP-----YRLPLGDVVGASRRTPMODSLRYARLGPFRRAFGKEFVWGA 81

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QY 56 RLKACDESRFDKLSQALKFVRDFAGDGLFTSMTEHKMKKANIILPESQAMKGY 115
D 82 ALAADLADDEAFAGHVGAVANLRVAGDGLFTAYNHENPMQLAHVDLAPFSNEMAGY 141
QY 116 HAMVNDIAVLQVOKERLNAD-EHI EYEDMTRLTLDTLGLCGFNENRNSYRDQHPFI 174
D 142 HVMMLDVAAARLTGHMDLAEASGRAVDYGDMTKLTLETIARTGFGHDSFERSRLHPFV 201
QY 175 TSMVRLADEAMNKLOKAN---PDDP-AVDENKROFGQDIAVMNDVXIIADSKA----- 225
D 202 TAMVGTIGYA---QRLNTPAPLAPMLLRDASRNADIAHLKRYDDLVERRANGCT 257
QY 226 -----SGEODDLTLHMLNGKDPETGEPLDDENIRYOIITFLIAGHETSGLSFALYFL 280
D 258 GCGTSGSGSGDLDRLMLETAPRTGERLSPQNRROQITFLVAGHETSGLSFALHYL 317
QY 281 VKNPHVLQKAAEAPARLVLD-PVPSYKOVKOLKTYGVNLALMLPAPAPSLYAKEDT 339
D 318 AQHBDVAAARAEVDRVWGDTAPGEQVAKLRVRRVLDLSRLMPTAPGFAAREABEDT 377
QY 340 VLGGSEPLEKGDLMVLIPOLHRDKITWGDVDEPRPERFENPSALPQ--HAFKPEGNGQ 397
D 378 VLGGTHPRRRGAMLVLTGMLHRDPEVWGADAERDPDRPAKAVRSAPHTFERPGTGA 437
QY 398 RACIGQOFALHEATLVLCMLKHEFEDHTNVELDIKETTLLKEGFFVAKAKSKIPLG 457
D 438 RACIGRQALHEATLVGLLRREYELREPEGRRLRVTERLTLMBEGLHLHVRR---TAA 494
QY 458 IPSPSTEOSAKVRKKAENAHNT 481
D 495 APAPGRTAAPGAADADAGTVSAP 518

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RESULT 4

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ID 060451 PRELIMINARY; PRT; 667 AA.
AC 060451;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE NADPH-cytochrome P450 oxidoreductase.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOLDEN;
RA Ohgita S., Gada T., Hoshino T., Shinzaki N., Kametaki T.;
RT "High-red yeast, construction of a novel strain of Saccharomyces
RT cerevisiae stably exerting high activity of hamster cytochrome P450
RT reductase.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; D83230; BA11856.1; -.
DR HSSP; P00388; IAMO.
DR InterPro; IPR003097; PAD binding.
DR InterPro; IPR001094; Flavodoxin-like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR Pfam; PF00667; FAD binding_1.
DR Pfam; PF00258; flavodoxin_1.
DR Pfam; PF00175; NAD binding_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
KM NADP.
SQ SEQUENCE 667 AA; 75850 MW; 2023FA3DF4C1EF07 CRC64;

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Query Match 14.2%; Score 773.5; DB 11; Length 667;
 Best Local Similarity 32.1%; Pred. No. 3.9e-40;
 Matches 210; Conservative 117; Mismatches 260; Indels 67; Gaps 25;

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QY 444 FVVAKSKKIPLG---IPSPTEOSA--KVRKKAENAHNTPLVLYSGNMGTAECTAR 498
D 31 FIRKKKEEVEPESKIOTATPSVKESFVEKMKKTGN-----IIVYGSQTGAEEFAN 85
QY 499 DLADIANSKAPAOVATLDSH---AGNLP--EGAVLYTASY-NGHPDNKAQFVDWL 551
D 86 RLAKDAHRYGMGMSADPEEYDLADLSLPEIKSLVFCMATYGEEDPDNDQFDYDWL 145
QY 552 DQASADKVKVRYSVFGCGKKNATTYQKVA---FIDETLAAGAENIDRGADSD 608
D 146 QETDVD-LTGKRAVFGNGK---IYENNAKGYVDRLBOLGAORITELGIDDDGN 200
QY 609 FEETSEWRHMSDVAAVFNLDIENSEDNKSTLSL--QFVSA---ADMPLAKNH-- 659
D 201 LEBDFITWRQFPNPAVCEFFGEVATGESSIRQYELLVHEDIDAAKYTTEMGRLKSYEN 260
QY 660 -----GAPSTNVASKELQOPGARSRLHETEL-PKEASTQESDHLGVIPRYEGT 710
D 261 QKPEFDANKPFLLAVTTNRKLNQ-GTERHLMHLELDISDKIRYESGDHVAVYPANDSTL 319
QY 711 VNRVTAFFGLDASQI---RLAEBEKLALPLAKTVSVELLYQVLELODPVTRTOLRAM 767
D 320 VNOIGETLGADLVVMSLNNLDESSNKHPRPCEPTTYRT-ALTYLDTNP-PRTNVLYE 377
QY 768 AAKTVCP-----HKVELALLEKQAYKEQVLAKRLTMLELEKYPACEMKSEFTALL 821
D 378 LAQYASPSPOEQOLHKMASSSGEKKELYLSMVVEARHIALIADYPSLRPIDHCELL 437
QY 822 PSIRPRYISISSBRUDEKASITVSVSGEAMSGEYGIASNYI-AELQSGDT--- 876
D 438 PRLQARYSIASSSKVHPNSVHICAVAVEAKSGRNV-KGVATSWRAKEPGENGRRA 496
QY 877 -ITCFISTPQSEFTLPMDPEPLIMVGPSTGVAPRFGVQARQOLKEQGSLSGAHLYFG 935
D 497 LVMEVVR--KSQRLPRKSVTPVIMVGPSTGVAPRFGVQARQOLKEQGSLSGAHLYFG 554
QY 936 CRSPHEDLYQOELENAQSEGIIT-LHTAFSRMNPQPTVVOHMEQDGKLTLELDQ-G 993
D 555 CRSDDELYLVRELIARHKQALQUNVAFSR-EQAHKYVVQHLKRDRLHMLKIHGG 613
QY 994 AHFYICDGSQMAPAVATLMKSYADYQVSEADARIMLOQLBEKRYADQWA 1047
D 614 AHIVVCGDARNMAKDVONTFYDIAEFGPMHQAADVVKMLTKRYSLDVS 667

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RESULT 5

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ID 040916 PRELIMINARY; PRT; 719 AA.
AC 040916;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4).
OS Pseudotsuga menziesii (Douglas-fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pseudotsuga.
OX NCBI_TaxID=3357;
RN [1]
RP SEQUENCE OF 1-44 FROM N.A.
RC STRAIN=(MIRB) FRANCO; TISSUE=SEEDLING;
RA Triabarger T.J., Misra S.;
RT "The molecular characterization of a set of cDNAs differentially
RT expressed during Douglas-fir germination and early seedling
RT development.";
RL Physiol. Plantarum 95:456-464 (1995).
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN=(MIRB) FRANCO; TISSUE=SEEDLING;
RA Triabarger T.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]

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Query Match	13.6%: Score 739.5; DB 10; Length 692;
Best Local Similarity	29.6%: Pred. No. 5, 7e-38;
Matches 196; Conservative 120; Mismatches 257; Indels 89; Gaps 19;	

Query	978 VMEDEGKLLIELDQGHAFITCGGSGOMAPAVEVTLTKSYADVQVSEADRLKLOOLEE 1037
Db	651 KITEKSGYVNIWLLAQGGYLVCGGAKAKMARDVHTLTHSIYVEQESVSTSAEATVKQLQT 710
Oy	1038 KGRYKADVW 1046
Db	711 EGRYLDVW 719

RESULT 6	Q9SB48	PRELIMINARY:	PRT:	692 AA.
ID	Q9SB48			
AC	Q9SB48			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-MAY-2002 (TrEMBLrel. 20, Last annotation update)			
DE	NADPH-FERRIHEMOPOTEIN reductase ATR1 (EC 1.6.2.4).			
GN	P22K18.280 OR A74G24520.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eustoids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bevan M., Wedler H., Wambutt R., Hohelsel J., Mewes H.W.,			
RA	Mayer K.F.X., Schueller C.;			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Wedler H., Wedler E., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Southgate A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,			
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,			
RA	Chauk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,			
RA	Kim C., Lin S.X., Narusaka M., Pham P.K., Sakano H.,			
RA	Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,			
RA	Ecker J., Theologis A., Davis R.W.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL093535; CAA23011.1; -			
DR	EMBL; AL161561; CAB79362.1; -			
DR	EMBL; AY054668; AAK96879.1; -			
DR	HSSP; P00388; IAMO.			
DR	InterPro; IPR003097; FAD binding.			
DR	InterPro; IPR001094; Flavodoxin like.			
DR	InterPro; IPR001226; Flavodoxin.			
DR	InterPro; IPR001709; FN_cyt_redctse.			
DR	InterPro; IPR001433; Oxred_FAD/NAD(P).			
DR	Pfam; PF00667; FAD_binding_1.			
DR	Pfam; PF00258; flavodoxin; 1.			
DR	Pfam; PF00175; NAD_binding_1.			
DR	PRINTS; PR00369; FLAVODOXIN.			
DR	PRINTS; PR00371; FPCR.			
KW	Oxidoreductase.			
SQ	SEQUENCE 692 AA; 76765 MW; 7DD7E418CF2FA6 CRC64;			

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Db      64 PKSLMAKDEDDDLG-----SKRTVSLFFGQTSTAGFAVAL 103
Qy      501 AD--IAMSFGAPQVATLDSHAGN-----LPREGAVLITYASY-NGHPDNKQPFVDM 550
Db      104 SEELKAREKAAVVIDDDYAADDDQYBEUKKETLAFVCAITYGDEPDMNARFKW 163
Qy      551 LDQASADEVK--GVRYSVFGCGDKMATTYQKVPFIDETLAAGAENIADRGADASDD 608
Db      164 FTEENERDIXLOALAYGFALGNROY--EHFNKIGIVLDEELCKGAKRILEVGLDDDDQS 222
Qy      609 FEGTYEERHEHMDVAAYFLND--IENSEDNKS-----TSLQ 645
Db      223 IEDFNMAKESLWBE-----LDKLLKDEDKSVATPYTAVIPYRVVTHDPRFTTQKSM 276
Qy      646 FVDSADWPLAKMGAFSTNVVASKELQPGSARSTRLEIPEKA--SYOEGHLYVIF 704
Db      277 ESNVANGNTTIDIHPCRVDAVQKELTHESDSCHELEPDISRTGITTYGTHVGYA 336
Qy      705 RNYEGIVNRTARFGLDASQOIRLEAEEKLAHLPLAKTVSV-----EELLQYVEL 755
Db      337 ENHVEIVEAGKLLGHSIDLVFSLHADKEDGS--PLESAVPPPPPGCTLTGLARVADL 394
Qy      756 QDPYTRQOLRAAKTVCPKHELEALLE--KOAYKEOVLAKRLTMLELLEKYPACEM 812
Db      395 LNPBKSLVALAAYATEPSEAEKIKULTSPDGDEYSQWIVASQRLLEVWAAFPSPAKP 454
Qy      813 KFSEFI--ALPSIRPRYSSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL--- 868
Db      455 PLGFYFALAIARLQPRYSSISSPRLASRVHTSALVYGPPTG--RIHKVCSTWMAKNA 513
Qy      869 --AEOEGDITTCFISTQSEFTLPKDPETPLIMVGTGVAPEPFGVQARQOLKEGOQ 925
Db      514 VPAKSHESGAPFIFIRA--SNFKLPSPNPTPIVMVGCGTGLAPRGLOERMALKEDE 571
Qy      926 SLGSAHLVFGCRSHEDLYOELENAQSEGIT--LHTAFSRMPQPTTYQVHMEODGK 984
Db      572 ELGSSLLFFGCRNQMDFIYEDELNPFVQGVISELIVAFSREGAQ--KEYVQHKMEKXA 630
Qy      985 KLIELLDGAFYICGDSQWAPAVEATLMKSYADVHQSADARLWLOLEKGRYAKD 1044
Db      631 QVMDLIKESGLVYCGDAKAGARVHRTLHTIVGQEBVSSEBAALVKKLQTEGRYLND 690
Qy      1045 VW 1046
Db      691 VW 692

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RESULT 7

048937 PRELIMINARY; PRT; 681 AA.

AC 048937; TREMBLrel. 06. Created)

DT 01-JUN-1998 (TREMBLrel. 06. Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20. Last annotation update)

DE NADPH cytochrome P450 reductase (EC 1.6.2.4).

GN PR2.

OS *Petroselinum crispum* (Parsley) (*Petroselinum hortense*).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Apiales; Apiaceae; *Petroselinum*.

OX NCBI_TaxID=4043;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98070859; PubMed=9405720;

RA Koopmann E., Hahlbrock K.,

RT "Differentially regulated NADPH-cytochrome P450 oxidoreductases in

RL *Parsley*."

DR EMBL; AF024634; AA897736.1; -.

DR HSSP; P00388; JMW.

DR InterPro; IPR003097; FAD_binding.

DR InterPro; IPR001094; Flavodoxin_like.

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DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FEN_cyt_reductase.
DR InterPro; IPR001433; Oxid_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1.
DR Pfam; PF00258; Flavodoxin_1.
DR Pfam; PF00175; NAD_binding_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR Oxidoreductase.
KW SEQUENCE 681 AA; 75674 MW; C67AD080E8BAE0F6 CRC64;

Query Match 13.5%; Score 737.5; DB 10; Length 681;
Best Local Similarity 30.7%; Pred. No. 7.4e-36;
Matches 200; Conservative 104; Mismatches 275; Indels 73; Gaps 18;

Qy 449 KSKKIPGGIPSPSTEQSAKVRKKAENANTPLVLYGSGNMGTAEGBARDLADIAKSG 508
Db 49 KSVPEPLIYPKYIEIEBVDGKK-----VTVEFGITGTABEFAPAFAPAEARARY 100
Qy 509 FAP--QVATLDSHA-----GNLPREGAVLITYASY-NGHPDNKQFVMDLQA--SA 556
Db 101 EKAFRVVDDDYAADEBEYEAKEKESFAFFFLATYGDGEPDMNARFYKWFSEGEKG 160
Qy 557 DEVKGVYVFGCGDKMATTYQKVPFIDETLAAGAENIADRGADASDDPEGTYEEN 616
Db 161 DWNKQLYGVFGLGNROY--EHFNKIAKVVDGLADQAKKIVEGMDDDQCIEDDTAW 219
Qy 617 REHMSD-----VAAYNLIDENSEDNKSTLSLOFVDSAA 651
Db 220 RELVPEPLDKLLDEDDTSAATPYTAVALERVVVYDQLTALDRSLSTONGHTVADA- 278
Qy 652 DMLAKMGAFASTNVVASKELQPGSARSTRLEIPEKA--SYOEGHLYVIFRNYEGT 710
Db 279 -----QHPQRS--SVAKKELHKKPASDRSCHELEPDISHTGLAYETGDHGVYCENLVEI 331
Qy 711 VNRTARFGDASQIRLEAEEKLAHL-----PLAKTVSVBELLQYVELQDPVTRTQ 763
Db 332 VEEAEKLLGQMPNTYFSVHDDDEGTPLTGSSLPPTCTVBSALAKVADLLSSPKSA 391
Qy 764 LRAWAAKTVCPKHELEALLE--KOAYKEOVLAKRLTMLELLEKYPACEMKFSEFIRA- 819
Db 392 LIALAAASPTEDRLRLASPGKDEYAGWVVASHSRLLEVLAEPSPAKPLGVFFAS 451
Qy 820 LLPISIRPRYSSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL---AEOEG-D 875
Db 452 VAPRLQPRYSSISSPPRDEKQASITVSVSGEAMSGYGEKGIASNYL---AEOEG-D 875
Qy 876 TITCFISTQSEFTLPKDPETPLIMVGTGVAPEPFGVQARQOLKEGOSLGEAHLVFG 935
Db 511 CSWAPIFVRQSNFPLPSDTPVPIIMIGTGLAPFRGLQERQALKAGAEGLTAVALYFG 570
Qy 936 CRSPHEDLYOELELN--AOSEGITLHTAFSRMPQPTTYQVHMEODGKLIJELDOGA 994
Db 571 CRNRLNDFIYEDELNKVESGISELIVAFSR--BGFKEYVQHKMLQKASEINWLIBEGA 629
Qy 995 HFYICGDSQWAPAVEATLMKSYADVHQSADARLWLOLEKGRYAKDVW 1046
Db 630 YIVYCGDAKAGARVHRLHTIAQEGALDSSAESVVKULQMTGRTLRDVM 681

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RESULT 8

08VX49 PRELIMINARY; PRT; 703 AA.

AC 08VX49; TREMBLrel. 20. Created)

DT 01-MAR-2002 (TREMBLrel. 20. Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21. Last annotation update)

DE Cytochrome P450 reductase (EC 1.6.2.4).

GN R2.

OS *Triticum aestivum* (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; *Triticum*.

Db 601 GCRRNRKDFIYEDLNNFVSGALSELVAFNR-EGPTKEYVQHKMOKASDINNMISQ 659
 Qy 994 AHFYICDGSQMAVAVENTLMKSYADVHOVSEADARLMLQOLEKGRYAKVM 1046
 Db 660 GYLVCDDAKGMADVHRALHTTVQEOGSLNKSSTESVSKLQNNGRILRVW 712

RESULT 10

Q39035 PRELIMINARY; PRT; 692 AA.
 ID Q39035
 AC Q39035;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE NMDPH-ferritin protein reductase.
 GN AT1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HEYNH; TISSUE=SEEDLING;
 RA Mignone-Vieux C., Kazmaier M., Lacroite F., Pompon D.M.;
 RL Submitted (May-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X66016; CAA46814.1; -
 DR HSBP; P00388; IAMO.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin-like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_reductase.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD binding; 1.
 DR Pfam; PF00258; Flavodoxin; 1.
 DR Pfam; PF00175; NAD binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR KMP.
 SQ SEQUENCE 692 AA; 76768 MW; 5E0216F008B5D49E CRC64;

Query Match 13.1%; Score 714.5; DB 10; Length 692;
 Best Local Similarity 29.2%; Pred. No. 2.1e-36;
 Matches 193; Conservative 119; Mismatches 261; Indels 89; Gaps 19;
 Qy 441 PEGFVNAKSKKIPGIPSPSTQSAKVKKAENANPTPLVLVYGSNMGTAAGTARDL 500
 Db 64 PKSLMADEDDDLG-----SKTIVSIFFGTGTAGFAKAL.103
 Qy 501 AD-IAMSKGAPQVATLDSHAGN-----LPREGAVLIVTASY-NGHPDPAKQFVDM 550
 Db 104 SEETKAREKAAKVYDLDYAADDDQYEELKKETLAFCAVATGDEPTDNARFSKM 163
 Qy 551 LDQASABEVK--GVRYSFGGCDKMATYQKVAFIDETLAAGAENIARGEADASDD 608
 Db 164 FTEENEDIKLQQLAYGFALGNROY-EHFNKIGIVDEELCKGAKLIEVGLDDQDS 222
 Qy 609 FEGYEEMREHMMSDVAAYFNLD-IENSEDNKS-----TLSDQ 645
 Db 223 IEDFPMKESLWSE-----LDKLLKDEDDKSVATPTAVIPRYVTHDPRTTQSM 276
 Qy 646 FVDSADWPLAKMHGAFSTNVVASKELQPGSASRSTRLELPKEA-SYQGDHLGYIP 704
 Db 277 ESNVANGNTTIDIHPRCVDVAVQKELHTHESDRSCILBFDISRTGITETGQHVGYA 336
 Qy 705 RNYGCIYVRVATARGLDASQOIRLEAEKELAHPLATTVSV-----ELLQYEL 755
 Db 337 ENHVEIYEBAKLLGSHLDLVSIAHAKEDS--PLESAVPPPPPGCTLTGLARVADL 394
 Qy 756 QDPTRTQRLAMAKTVCPKHELEALE---KQAYKEOVLAKRLTMLLEKYPACEM 812
 Db 395 LNPFRKSLVALAAVATPSEAEKLLHTLSPDGKDEYSQWIVAGORSILLEVMAAPSPAKP 454

Qy 813 KFESEFI-ALLPSIRPRYSSSPRDEKASITTSVSVSEAMSGCEYIGIASNYL--- 868
 Db 455 PLGVFFAALIPRLQPPRYSSSCODWAPSRVHTSALVYGPPTG-RHHGVCSTWAKNA 513
 Qy 869 ---AEIQEGDTICPSTPQSEFTLPKDPETPLIMGPGGVAPFGFVQARQOLKEQG 925
 Db 514 VPAKSHGSCGATIFIRA--SNKFLPSNPSTPIVMQPGTGLAPFGFLOERNALEDGE 571
 Qy 926 SLGEAHLVFCGRSPHEDLYQEELENAQSGIIT-LHTAFSRMNPQKTYVQHVMEQDGK 984
 Db 572 ELGSSILFFGCRNRQMDFIYEDLNNFVDCGVISELIMAFSRGAQ-KEYVQHKMEKAA 630
 Qy 985 KLIELDQGNHFIYICDGSQMAVAVENTLMKSYADVHOVSEADARLMLQOLEKGRYAKD 1044
 Db 631 QVMDLKEEGYLYCGDAKGMADVHRALHTTVQEOGESSSEAEALVKRLQTEGRYLRD 690
 Qy 1045 VM 1046
 Db 691 VM 692

RESULT 11

Q24424 PRELIMINARY; PRT; 683 AA.
 ID Q24424
 AC Q24424;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE NMDPH-ferritin protein reductase (EC 1.6.2.4).
 OS Papaver somniferum (Opium poppy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Papaveraceae; Papaver.
 OC NCBI_TaxID=3469;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98096363; PubMed=9434750;
 RA Rosco A., Pauli H.H., Priesner W., Kutchan T.M.;
 RT "Cloning and heterologous expression of NMDPH-cytochrome P450
 reductases from the Papaveraceae";
 RT Arch. Biochem. Biophys. 348:369-377(1997).
 RL Arch.
 DR EMBL; U67185; AAC05021.1; -
 DR HSBP; P00388; IAMO.
 DR InterPro; IPR003097; FAD binding.
 DR InterPro; IPR001094; Flavodoxin-like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_cyt_reductase.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD binding; 1.
 DR Pfam; PF00258; Flavodoxin; 1.
 DR Pfam; PF00175; NAD binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 DR KMP.
 SQ SEQUENCE 683 AA; 75888 MW; E07BD5E5EADBE002 CRC64;

Query Match 13.0%; Score 711.5; DB 10; Length 683;
 Best Local Similarity 30.3%; Pred. No. 3.2e-36;
 Matches 191; Conservative 113; Mismatches 263; Indels 63; Gaps 20;

Qy 470 VRKKAENANPT---LLVLVYGSNMGTAAGTADLAD-IAMSKGAPQVATLDSHAG-- 521
 Db 64 IDKEEIEIEVDPGIKTLTFFGTGTAGFAKALAEIKAKYKAVKAVKVDLDYVAED 123
 Qy 522 ---LPREGAVLIVTASY-NGHPDPAKQFVDMDO--ASADDEVGVAVYSGCGDKN 573
 Db 124 DQYEELKKESLVPFWATYGDEPTDNARFKWFTQEHREGSWLQQLTYGVFGLGNRO 183
 Qy 574 MATYQKVPAFIDETLAAGAENIARGEADASDEGTEEMREHMMSD----- 623
 Db 184 Y-EHFNKINADVDEQKQAKRIYQVGLGDDQCIEDPTARRELLMTLDDQLKXEDA 242
 Qy 624 -----VAAYFNLDIENSEDNKSTLSLQFVDSA-ADWPLAKMHGAFSTNVVASKELQ 674


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Db      243 ABSVATPIYITVDEYRVHIEHTVAALDDHINTANGDVAADILHPC-RTTVAQOERLAK 301
Qy      675 PGASARSTRHLEIEP--KEASYOEGDHLGVI PRNVEGIVNVTARFG--LDASQOIRLEAE 731
Db      302 PKDRSCGHIHEFDLSSSSLYTETGDHGVYAENDEVEEAGKLLGGPDLPLPSIHDK 361
Qy      732 EEKLAHLPLAKTVSV-----EELLQYVELQDPVTRTQRLAMAAKTVCPPHKYLEA 782
Db      362 DGS-----PGSSLPPEPPGCTLRALSALARYADLINPRKASLIALSAHVASPSEARLRF 417
Qy      783 L-----LEKQAYKEQYLAARLMTLELEKYPACEMKFSFEI--ALLPSIRPRYSSISSSRVD 838
Db      418 LSSPLGKNNESKMWVGSQRLLEITMAEPFSAKPPPLGVFAAVARLPRRYSISSSPKFA 477
Qy      839 EKASITVSVSGEAMSGEYEGKIASNYLAELQEGT-ITCFISTQSEFTLPKDETP 897
Db      478 PSKIHVTCALVYGOSPTG-RVHRGVCSTWKKHAPQDSMAPIFRT--SNFKLPADSTP 534
Qy      898 LINVPGCTGVAAPRFGVQARQKQLEKQOSLGEAHLVFCRSPHEDVLYOELENAQSEGI 957
Db      535 IIMVGPCTGLAPFRGFLQERWALKENGALQGPVAVLFGCRNRNMDFIYEDELNNFVERGV 594
Qy      958 IT-LHTFESMPNPKTYVQVHWEQDGKLLIELDQAHFYICGDSQMAPVEATLMKS 1016
Db      595 ISELVIAFSR-EGEKKEYVGHKMEKATDVWNVISGQDYLVCADAKMARVHRTLHTI 653
Qy      1017 YADVHGVSEADARLMLQOLEEKGRYAKDV 1046
Db      654 AQOEGPMESSAAEAAYKQLQVEERYLRD 683

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RESULT 12

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Q9AU08 ID Q9AU08 PRELIMINARY; PRT; 692 AA.
AC Q9AU08;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DE NADPH-cytochrome P450 oxidoreductase isoform 1.
OS Populus balsamifera subsp. trichocarpa x Populus deltoides.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OC NCBI_TaxId=3695;
RN [1]
RP SEQUENCE FROM N.A.
RA Ro D.-K., Douglas C.;
RT "Functional characterization of cytochrome P450 reductase from the
RT hybrid poplar (Populus trichocarpa x P. deltoides).";
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF02496; AAK15259.1; -.
DR HSSP; P00388; 1MO.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1.
DR Pfam; PF00258; Flavodoxin_1.
DR Pfam; PF00175; NAD_binding_1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
SQ SEQUENCE 692 AA; 76725 MW; 7AA8CC7AB3C984D9 CRC64;

```

Query Match

Best Local Similarity 13.0%; Score 711.5; DB 10; Length 692;
Matches 199; Conservative 110; Mismatches 252; Indels 127; Gaps 20;

```

Qy      431 LDIKETLTLKPEGVVAKSKKILGLIPSPSTQSKAKYRKAKENAHNPLVLVYGSNM 490
Db      60 LVVFKSLISIDE-----EDSEALGG-----KTKVTLFYGTQT 92

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Qy      491 GTAEGTARLAD--TMSKGFAPQVATLDSHA-----GNLPRGAVLITVASY--NGHP 540
Db      93 GTAEAGKALAEVKAARYEKAAYKAVFDLDYAMEDDQYEEKLKKETLALFMVATYDGB 152
Qy      541 PDNAKQFVWMLDQASADVE--KGVRSYVFCGCGKMMATTYOKYAPAFIDETLAKGAEIN 598
Db      153 TDNAARFYKWFTEGNRGITWLOOLSYVFLGKRQY-EHFNKIAKVDDLTYQGGKRLV 211
Qy      599 DRGEADASDDEFEETYEEMEHMWSDVAAAFNLDIENSEDNKSTLSQFVDSADMPLA-- 656
Db      212 PVGLGDDQDCEIDDFSAKKEFLWPELD-----QLNDEDDVNAFSPYTAIPEYLVH 266
Qy      657 -----KMGAFSTNVASKLOQPGASRSTRHLEIEPKA-SY 694
Db      267 DPSIISVEDKFSNLIANGVNSFDIHPCRVVAVAQKEHLHAESDRSCIHLEFDITGITY 326
Qy      695 QEBDHLGVIPRNVEGIVNVTARFGDAEQIRLBAEBEKLALPLAKTVSV----- 747
Db      327 ETGDHLGVYAENSDEVE-----EAGKLDKPLDLLFSIHADNEDGT 368
Qy      748 -----EELQYVELQDPVTRTQRLAMAAKTVCPPHKYLEALB---K 786
Db      369 AIGSSLPPEPPGCTLHTALACYADLLSPKKAALLALAAHASEPSEADRLKFLSSPQK 428
Qy      787 QAYKEQYLAARLMTLELEKYPACEMKFSFEI--ALLPSIRPRYSSISSPRVDEKQASIT 845
Db      429 NEYSHWMAVSQRLLEITMAEPFSAKPPPLGIFFAVAPRLQPRYSSISSSPRYPNRVHVT 488
Qy      846 VSVSGEAMSGEYEGKIASNYL---AEQEGTITCF---ISTPSEFTLPKDETPPLI 899
Db      489 CALVGPPTPG-RIHNGVCSWKKHAPVLEK--SYCSMAPIFRTSNFGLPADSTPIL 545
Qy      900 MVGPCTGVAAPRFGVQARQKQLEKQOSLGEAHLVFCRSPHEDVLYOELENAQSEGIIT 959
Db      546 MVGPCTGLAPFRGFLQERWALKENGALQGPVAVLFGCRNRNMDFIYEDELNNFVEGIVS 605
Qy      960 -LHTAFSMPNPKTYVQVHWEQDGKLLIELDQAHFYICGDSQMAPVEATLMKSYA 1018
Db      606 ELIVASREBPQ-KEYVGHVWVRAAEIWTIISQGVFYVCGADAKMARVHRTLHTIVQ 664
Qy      1019 DVHGVSEADARLMLQOLEEKGRYAKDV 1046
Db      665 EGGGLSSKTESWVKLQMEGRYLRD 692

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RESULT 13

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Q43235 ID Q43235 PRELIMINARY; PRT; 692 AA.
AC Q43235;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DE NADPH-ferritinoprotein reductase (EC 1.6.2.4).
OS Vicia sativa (Spring Vetch) (Tare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Vicia.
OC NCBI_TaxId=3908;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VAR. LOLITA; TISSUE=SEEDLING;
RA Benveniste I., Begue-Klim C., Lesot A., Hasenfratz M., Duret F.;
RT "Isolation and characterization of a cDNA encoding an NADPH-cytochrome
RT P450 reductase from Vicia sativa.";
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
DR EMBL; Z26252; CAAB1211.1; -.
DR HSSP; P00388; 1J92.
DR InterPro; IPR003097; FAD_binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR001226; Flavodoxin.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1.

```

DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00175; NAD binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 KM NADP; Oxidoreductase.
 SQ SEQUENCE 692 AA; 76912 MW; 49CB4AEC611BB99 CRC64;

Query Match 13.0%; Score 711; DB 10; Length 692;
 Best Local Similarity 28.4%; Pred. No. 3.5e-36;
 Matches 198; Conservative 120; Mismatches 287; Indels 92; Gaps 21;

QY 406 ALHATVILGMLKHPEDHTNVELDKETLTKPEGFVVKASKIPLGIGSPSTEQ 465
 DB 32 ATTSAAVIGLLV--FLMRKSPDRSRRLRPVIVK--FTYKHDDEVEV----- 76
 QY 466 SAKVRKKAENAHNTPLLVYGSNMGTAEAGTARDL--IAMSGFAPQVATLDSA--- 520
 DB 77 -----DRGITKTVTFYGTGTGTAEAGTAKALAEIKARYEKAVVKKVDMMDYALDD 126
 QY 521 ----GNLPREGAVLIVTASY--NGHPDNKQFVMDLQASAD--VKYRVSVFGGDK 572
 DB 127 DQVEKLKKEKTLVFFMLATYGDGEPTDAAAFYKMFTEGKEEGTWMQLTYGVFALGNR 186
 QY 573 NMATYQKVPFIETLAKAENIADRGENDASDDEPGTGEERHEHMSDVAAVFNLDI 632
 DB 187 QY-EHFNKIKGIVDEDLTEOGAKRLVPVGLDDQSIEDENAKETLMPELD-----QL 240
 QY 633 ENSDNKSTLSLOFVDSADWPLA-----KMGAFSTNVVAS 669
 DB 241 LRDDDDVNTASTPTTAISERVVITHPTVSPYENHFNVANGAVPDIIHPCVNVNAV 300
 QY 670 KELQPGASARSTRHLELP--KEASYOEGHGLVYPRNVEGIVNRVTAFFGLDASQOIRL 728
 DB 301 RELHKPOSDRSCIHLEFDLSGTGVTETGHDVGAENCDTEVEAGKLLGSLDLFSL 360
 QY 729 EAEKELKHL-----PLAKTVSVBELQ--YVELQDPTRTQLAAMAKVCPHNYELE 781
 DB 361 HTDEDDSTLSGSLPPPPGCTVRTALACADYDLNPRKAAIYALAAHSEPEABRLK 420
 QY 782 ALLE---KQAYKEOVLAKRLTMLLEKYPACEMKFESEFI--ALLPSIRPRYSSISSPRV 837
 DB 421 FLSPQKDEYSKVVNSQSLLEVMADEPFAKAPPLVGFPAIAPRLOPRYSSISSPR 480
 QY 838 DEKQASITVSVAEANSYGVEYKGIASNYLAEL---QEGDTITCFISTPQSEFTLPKD 893
 DB 481 APQVHTVTCALVEGPPTG--RIHKGVCSITWKSATPLEKSHDCSRAPFIFIRSPKLPAD 539
 QY 894 PETLLINVGPTGVAPFRGFVQARKQLKEQOSIGEAHLVFGCRSPHEDVYQSELENAQ 953
 DB 540 HSITINVGPTGLAPFRGFLQERIALKEDEVOLGPAULFPGCCRRNQRMDFIYEDLNFFV 599
 QY 954 SEGIIT-LHTFSRMPNQPTVVOHVMEQDKLIELLDGAHFYICGDSQMAPAVEAT 1012
 DB 600 QQGAISELIVAFSR--EGPEKEVVOHKMDKAEYMLSLISQSGIYVCGDAGKMDVHRS 658
 QY 1013 LMKSYADVHQVSEAD--ARLMLQOLEEKGRAVDW 1046
 DB 659 L---HTIVQOENADSSKAEATVKKLQMDGRYLRDW 692

RESULT 14
 Q9FWM7 PRELIMINARY; PRT; 656 AA.
 AC Q9FWM7;
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE NADPH-cytochrome P450 reductase (Fragment).
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticaceae; Triticum.
 NCBI_taxid=4565;

RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=CV. DARIUS;
 RX MEDLINE=20322901; Pubmed=10864454;
 RA Barard Y., Hohn A., Nedelkina S., Schalk M., Pallett K., Schaller H.,
 RA Werck-Reichhart D.,
 RT "Increasing expression of P450 and P450-reductase proteins from
 RT monocots in heterologous systems."
 RL Arch. Biochem. Biophys. 379:161-169(2000).
 DR EMBL; AF123610; AAC17471.1; .
 DR HSSP; P00388; 1AM0.
 DR InterPro; IPR003097; FAD_binding.
 DR InterPro; IPR001094; Flavodoxin_Like.
 DR InterPro; IPR001226; Flavodoxin.
 DR InterPro; IPR001709; FPN_Cyt_reductase.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00667; FAD_binding_1.
 DR Pfam; PF00258; flavodoxin; 1.
 DR Pfam; PF00175; NAD_binding; 1.
 DR PRINTS; PR00369; FLAVODOXIN.
 DR PRINTS; PR00371; FPNCR.
 FT NON TER 1
 SQ SEQUENCE 656 AA; 72950 MW; E73E3BD3DA8485F5 CRC64;

Query Match 13.0%; Score 710; DB 10; Length 656;
 Best Local Similarity 29.5%; Pred. No. 3.7e-36;
 Matches 197; Conservative 109; Mismatches 264; Indels 98; Gaps 23;

QY 448 AKSKTIPLGISPTSTEQSAKKVRKKAENAHN--TPLLVYGSNMGTAEAGTARDLADIAM 505
 DB 18 APPKPPASFRPP-----VKVDADDGDKRRTVTFYGTGTAEAGTAKALAEIK 69
 QY 506 SK--GFAPQVATLDSHAG-----NLPRGAVLIVTASY--NGHPDNKQFVMDLQAS 555
 DB 70 ARYEKVLKTVDDDDVAAEDDEVEBEKTKETPLPLATYGDGEPTDAAAFYKMFTEGK 129
 QY 556 ADEV--KGVRYVPGCGDKMATTYQKVPFIETLAKAENIADRGENDASDDEPGTY 613
 DB 130 EKEVWLKDFNVYAVFGINROY--EHFNKVAKEVDELLLEQGNLVPVGLDDQCIEDDF 188
 QY 614 EEMREHMSD-----VAAVFNLDIENSDNKTLSLOFVDSAD 652
 DB 189 TAMKELVPELDDLLRDEDDTGAATPTTAIRYRVFIDKSD-----LEEDS-- 239
 QY 653 MPLAKMHGAS-----TNVASKELQPGASARSTRHLELPKEA--SYOEGHGLVYPR 705
 DB 240 WTLANGNGVDAQHPGCAVNAVVKELKRPASDSCIHLEFDISGTGLVETGHDVGYSE 299
 QY 706 NYEGIVNRVTAFFGLDASQOIRLEABEE-----KLAHLPLAKTVSV--ELQYVEL 755
 DB 300 NSIETVQAEFTLLDSPDTVFSIHADAEDSPKGGGSLAP--PPSPCTRTALRYADL 358
 QY 756 QDPVTRTQLAAMAKVCPHNYELELLE---KQAYKEOVLAKRLTMLLEKYPACEM 812
 DB 359 LNPCKKALTALAAHSDPTEABRLRFLASPAQDETAQMTIVASQSLLEVMAAFPAKP 418
 QY 813 KFSEFI--ALLPSIRPRYSSISSPRVDEKQASITVSVAEANSYGVE-----YKGIAS 865
 DB 419 PLGVFFAIAIPRIQPRYSSISSPKLAPRIHTCALV-----YGPRTTBRIHQVCS 471
 QY 866 NYLAEL-----QEGDTITCFISTPQSEFTLPQDPTPLINVGPTGVAPFRGFVQARKQ 919
 DB 472 TMMKNLTLPLEYSECSWAPIFVR--QGNFRLPADPSTPIIMIGPTGLAPFRGFLQERLA 529
 QY 920 LKEGQSLGEAHLVFGCRSPHEDVYQSELENNQSEGIIT-LHTAFSRMNPQKTYOVH 978
 DB 530 LKSGAELGSSVVFPGGRNEMDPIYEEELQNLQSEALSELVVAISR--BGPTREYQHK 588
 QY 979 MEQDGKLLILLDQGAHFYICGDSQMAPAVEATLMKSYADVHQVSEADARLMLQOLEEK 1038
 DB 589 MVDKATIEINVIQSGGIYVCGDAGKMDVHNLHTIVQKQSLDSKTEIVYKXNLQME 648
 QY 1039 GRVAKDWM 1046

Db 649 GRYLBDVW 656

RESULT 15

Q9SUM3 PRELIMINARY; PRT; 711 AA.

AC Q9SUM3; 01-MAY-2000 (TREMBLER1.13, Created)

DT 01-MAY-2000 (TREMBLER1.13, Last sequence update)

DE 01-MAY-2002 (TREMBLER1.20, Last annotation update)

DE MADPH-FERRIHEMOPROTEIN reductase (ATR2) (EC 1.6.2.4).

GN FN11.60 OR AT4G30210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN

RP SEQUENCE FROM N.A.

RA Meyer M., Kalicki J., Wohlmann P., Smith A., Bancroft I., Mewes H.W.,

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

RP Arabidopsis sequencing project;

RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Kalicki J., Wohlmann P., Smith A., Mewes H.W., Lemcke K.,

RA Meyer K.F.X.;

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

RA Palm C.J., Theologis A., Ecker J., Davis R.W.;

RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL109796; CAB52465.1; -

DR EMBL; AL161576; CAB81014.1; -

DR EMBL; AF325101; AK17169.1; -

DR HSSP; P00388; IAMO.

DR InterPro; IPR003097; FAD binding.

DR InterPro; IPR001094; Flavodoxin-like.

DR InterPro; IPR001226; Flavodoxin.

DR InterPro; IPR001709; FPN_Cyt_redctse.

DR InterPro; IPR001433; Oxired_FAD/NAD(P).

DR Pfam; PF00667; FAD binding; 1.

DR Pfam; PF00258; Flavodoxin; 1.

DR Pfam; PF00175; NAD binding; 1.

DR PRINTS; PR00369; FLAVODOXIN.

DR PRINTS; PR00371; FPNCR.

KM Oxidoreductase.

SO SEQUENCE 711 AA; 78927 MW; F0503108EB7F508F CRC64;

Query Match 13.0%; Score 709; DB 10; Length 711;
Best Local Similarity 28.4%; Pred. No. 4.9e-36;
Matches 190; Conservative 120; Mismatches 264; Indels 96; Gaps 20;

Qy 434 KETTLKPEGVVAKSKIPGLGIPSTEQSAKVKKAKENAHNTPLVLVYGSNMGT 493
Db 81 KRVEPLRP--LVIRPREELIDG-----RKK-----VTIFRGTGT 116
Qy 494 EGTARDIADIAMSKGFAP--QVATLDSHAGN-----LPREGAVLIVTASY-NGHPPDN 543
Db 117 EGFAKALGEAKAKAYEKTRFKIVLDYAADDEYEKLLKKEDEVAFPLATYGDGEPDN 176
Qy 544 AKQFVMDLDQAS--ADSVKGRYSVFGGDDKNMATTYQKVPATIDETLAAGAENIADRG 601
Db 177 AARFYKWFTEGNDGEWLKIKYGVFGIGNROY-EHFNKAVKVVDDIIVEQAGRLVQVG 235

Qy 602 EADASDDEFTYEERHEHMSDV-----AAVENDLIDNSDNTSTL 642
Db 236 LGDDDCIEDDEFTAMREALMPELDTILREEDTAATPYTAALVYVSIHSDAKFN- 294
Qy 643 SLOFVDSAAAMPPLAKMKG-----AFSTNVASKELQPGSARSRHRHIELPKKA-S 693
Db 295 -----DINNANGGVTVFPAQHPYKANVAKRELHPESRSCIHLEFDIAGGLT 345
Qy 694 YOECDHLGVIPIRYVEGIVNHTARFGUDASQOIRLEAEERKLAHLPLAKTVSV----- 746
Db 346 YETGDHVGVLCDNLSEVDALRLDMSPTDYSIHAERKD--CTPISSSLPPFPFPCNL 403
Qy 747 -EBILOVELQDPYRTQILAMAAKTVCPHXYELEALL- -KOAYKEOVLAKRLTME 802
Db 404 RIALTRYACLLSPKKSALVALAAHSDPTEAERLKLASPAKDEYSKWVESQRSILE 463
Qy 803 LLEKYPACEMKFSFILA-LPISIRPRYYSISSSRVDEKASITVSYSVGEAMSGYEYK 861
Db 464 VMAEFPSAKPPLGVFFAGVAPRLQPRFYSISSPKIAETRIHVICALVYEMPTG-RHK 522
Qy 862 GIASNYLAELQEGDITICFISTP-----QSEFTLPKQDETPLINVGPGTVAPFRGFQAR 917
Db 523 GVCSTMKNAPPYEKSENCSSAPLPIVQSNFKLPDSKVPIMIGPGLAPFRGFIQER 582
Qy 918 KOLKEQOSLGEAHLYPECRSPHEDVLYOELEN-AQSEGIITLHTAFSRMPNQKTYVQ 976
Db 583 LALVESGVLELGPVLFPGCNRMRDPIYEBELQRFVESGALAEISVAFSR-EGPTKEYVQ 641
Qy 977 HWNEQDKLIELLDQAHFYICGDSQMAPAYEATIMKSYADVHQVSEADARMLQOLE 1036
Db 642 HKWMDKASDIWNMISQAYLYVCGDAKMAVDHRSHTTIAEQGSMDSTVAEGFVNLO 701
Qy 1037 EKGRYAKDVW 1046
Db 702 TSGRYLRDVW 711

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